

GenCore version 5.1.6  
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OM protein - protein search, using sw model

Run on: September 23, 2005, 09:44:30 ; Search time 72 Seconds  
(without alignments)  
1058.219 Million cell updates/sec

Title: US-10-077-406-1  
Perfect score: 1133  
Sequence: 1 SQQAVPPYASENQTCRDOE.....QSDTTCKNPLEPLPPMSGT 197

Scoring table: BLOSUM62

Gapop 10.0 , Gapext 0.5

Searched: 2105692 seqs, 386760381 residues

Total number of hits satisfying chosen parameters: 2105692

Minimum DB seq length: 0

Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%  
Maximum Match 100%  
Listing first 45 summaries

Database : A\_Geneseq\_16Dec04:\*

1: Geneseqp1980s:\*

2: Geneseqp1990s:\*

3: Geneseqp2000s:\*

4: Geneseqp2001s:\*

5: Geneseqp2002s:\*

6: Geneseqp2003as:\*

7: Geneseqp2003bs:\*

8: Geneseqp2004s:\*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	DB ID	Description
1	1133	100.0	197	2	Aaw23220 Extracell
2	1133	100.0	197	2	Aay31326 Human lym
3	1133	100.0	197	8	Ado43009 Lymphotox
4	1133	100.0	305	8	Adj67643 Human ova
5	1133	100.0	435	6	Abp96137 Human TNF
6	1133	100.0	435	6	Abp96137 Human TNF
7	1133	100.0	435	6	Abp96137 Human TNF
8	1133	100.0	435	7	Abp96137 Human TNF
9	1133	100.0	435	7	Abp96137 Human TNF
10	1133	100.0	435	7	Abp96137 Human TNF
11	1133	100.0	435	8	Abm81346 Tumour-as
12	1133	100.0	435	8	Abm81346 Tumour-as
13	1133	100.0	446	8	Abm81346 Tumour-as
14	1133	100.0	450	8	Abp96137 Human TNF
15	1129	99.6	399	6	Abp96137 Human TNF
16	1129	99.6	399	8	Abp96137 Human TNF
17	1129	99.6	410	8	Abm81346 Tumour-as
18	1122	99.0	293	8	Adp81157 Protein o
19	1122	99.0	635	8	Adj67641 Human ova
20	1122	99.0	635	8	Adj67641 Human ova
21	1108	97.8	416	7	Adc42856 REMAP pro
22	1091	96.3	361	8	Adj67637 Human ova
23	1091	96.3	361	8	Adj67637 Human ova
24	987	87.1	170	6	Ada49700 Extracell
25	981	86.6	170	7	Adl17745 human Lym

26	970	85.6	172	8	ADJ56818	Adj56818 Human LTB
27	771	68.0	402	7	ABM85508	ABM85508 Mouse pro
28	771	68.0	415	4	ABM85508	ABM85508 Human tum
29	771	68.0	415	6	ABP96138	ABP96138 Mouse lym
30	771	68.0	415	7	ADP18289	ADP18289 TIL5 recep
31	771	68.0	415	8	ADJ96157	ADJ96157 Human LTB
32	756	66.7	166	8	ADP81159	ADP81159 Protein o
33	456	40.2	77	2	Aaw94642	Aaw94642 TNF-R ext
34	456	40.2	77	4	ABM85509	ABM85509 Human TNF
35	381.5	33.7	305	5	ABP41926	ABP41926 Human ova
36	381.5	33.7	305	8	ADP81160	ADP81160 Protein o
37	315	27.8	518	2	AAR51003	AAR51003 Sequence
38	311.5	27.5	659	6	ABJ37103	ABJ37103 Concatame
39	311.5	27.5	659	8	ADQ79910	ADQ79910 Human tum
40	309	27.3	461	2	AAR72504	AAR72504 p75 Tumou
41	307	27.1	720	6	ABJ37101	ABJ37101 Concatame
42	307	27.1	720	8	ADQ79906	ADQ79906 Human tum
43	305	26.9	225	3	AAY77463	AAY77463 Primate p
44	305	26.9	225	6	AAO26526	AAO26526 Human tum
45	305	26.9	227	4	AAB66981	AAB66981 Tnfr2 pro

ALIGNMENTS

RESULT 1

AAW23220

ID AAW23220 standard; protein; 197 AA.

XX AC AAW23220;

XX XX

DT 29-OCT-1997 (first entry)

XX XX

DE Extracellular domain of human lymphotoxin beta receptor.

XX XX

KW Human, lymphotoxin beta; receptor; blocking agent; extracellular;

KW ligand binding; domain; treatment; Th1 cell; immune response; delayed;

KW hypersensitivity; contact; tuberculin; granulomatous; graft versus host;

KW disease; organ rejection; autoimmune; disorder; multiple sclerosis;

KW insulin dependent diabetes; uveitis; cytokine; sympathetic ophthalmia;

KW psoriasis; Listeria; Toxoplasma; infection; Mycobacterium; abnormal;

KW lymphoid organ; development.

XX OS Homo sapiens.

XX XX

PN WO9703687-A1.

XX XX

PD 06-FEB-1997.

XX XX

PF 19-JUL-1996; 96WO-US012010.

XX XX

PR 21-JUL-1995; 95US-00505606.

XX XX

PA (BIOJ ) BIOGEN INC.

XX XX

PI Browning JL, Benjamin CD, Hochman PS;

XX XX

DR WPI, 1997-132373/12.

XX XX

PT Compositions comprising lymphotoxin-beta receptor blocking agent - used

PT to treat autoimmune diseases, e.g. sclerosis, insulin-dependent

PT diabetes, etc.

XX XX

PS Example 1; Page 55-56; 76pp; English.

XX XX

CC The present sequence, a human lymphotoxin beta receptor (LT-beta-R)

CC blocking agent, comprises the extracellular ligand binding domain of the

CC human LT-beta-R up to the transmembrane region. It can be used to treat a

CC Th1 cell mediated immune response which contributes to a delayed type

CC hypersensitivity reaction, preferably contact, tuberculin type or

CC granulomatous hypersensitivity, graft versus host disease, organ

CC rejection or an autoimmune disorder, i.e. multiple sclerosis, insulin

CC dependent diabetes, sympathetic ophthalmia, uveitis and psoriasis. It can

Lee, B.  
10/077406  
Seq. ID 1

CC also be used to treat conditions exacerbated by the activities of Th-1  
 CC type cytokines, or *Listeria*, *Toxoplasma* or *Mycobacterium* infection. Its  
 CC ability to selectively or partially block the LT-beta-R pathway may be  
 CC useful in the treatment of abnormal lymphoid organ development associated  
 CC with misexpression or overexpression of signalling by the LT-beta-R  
 CC pathway. The present LT-beta-R blocking agent is capable of selectively  
 CC inhibiting Th1, but not Th2 cell dependent immune effector mechanisms. As  
 CC Th1 cytokines can inhibit Th2 cell dependent responses, the present LT-  
 CC beta-R blocking agent may also indirectly stimulate certain Th2 cell  
 CC dependent responses which are normally inhibited by Th1 induced  
 CC cytokines. Doses of about 1 mg/kg of the present soluble LT-beta-R are  
 CC expected to be suitable starting doses for optimising treatment  
 XX  
 SQ Sequence 197 AA;

Query Match 100.0%; Score 1133; DB 2; Length 197;  
 Best Local Similarity 100.0%; Pred. No. 1.2e-78;  
 Matches 197; Conservative 0; Mismatches 0; Indels 0; Gaps 0;  
 QY 1 SQQAVPPVASENOTCRDQKEYEYEPQHRICCSRCPPGTYVSACKSRIRDVTVCATCAENS 60  
 DB 1 SQQAVPPVASENOTCRDQKEYEYEPQHRICCSRCPPGTYVSACKSRIRDVTVCATCAENS 60  
 QY 61 YNEHWNLYTICQLCRPCDPVMGLEEIAPTCKRKTQCRQCPGMFCAAWALECTHCELLSD 120  
 DB 61 YNEHWNLYTICQLCRPCDPVMGLEEIAPTCKRKTQCRQCPGMFCAAWALECTHCELLSD 120  
 QY 121 CPPGTEAELKDEVGKNNHCVPCKAGHFQNTSSPSARCQPHTRCENQGLVEAAPGTAQSD 180  
 DB 121 CPPGTEAELKDEVGKNNHCVPCKAGHFQNTSSPSARCQPHTRCENQGLVEAAPGTAQSD 180  
 QY 181 TTCKNPLEPLPPEMSGT 197  
 DB 181 TTCKNPLEPLPPEMSGT 197

RESULT 2  
 AAY31326  
 ID AAY31326 standard; peptide; 197 AA.  
 XX  
 AC AAY31326;  
 XX  
 DT 04-OCT-1999 (first entry)  
 DE Human lymphotoxin (LT)beta-receptor extracellular region.  
 XX  
 KW Lymphotoxin-beta; LT-beta; LT-beta receptor; follicular dendritic cell;  
 KW immune system; tumour; follicular lymphoma; extracellular domain; human.  
 OS Homo sapiens.  
 XX  
 FN WO938525-A1.  
 XX  
 PD 05-AUG-1999.  
 XX  
 PF 29-JAN-1999; 99WO-US001928.  
 XX  
 PR 30-JAN-1998; 98US-0073112P.  
 PR 02-FEB-1998; 98US-0073410P.  
 XX  
 PA (BIOJ ) BIOGEN INC.  
 XX  
 PI Browning J, Thorbecke J, Tsiagbe V;  
 XX  
 DR WPI; 1999-469242/39.  
 XX  
 PT New method of treating follicular lymphomas by inhibiting interaction  
 PT between lymphotoxin-beta and its receptor.  
 XX  
 PS Example 1; Page 25-26; 31pp; English.  
 XX  
 CC The invention provides a method for arresting or reducing, severity of  
 CC effects of a tumour by administration of a composition which inhibits the

CC interaction between lymphotoxin (LT)-beta and its receptor. An inhibitor  
 CC of the interaction between LT-beta and its receptor can be administered  
 CC for altering the survival or maintenance of follicular dendritic cells in  
 CC a subject and for altering the architecture of the organs of the immune  
 CC system. The method is useful for treating tumours, specifically  
 CC follicular lymphomas. It offers an alternative therapy for those with  
 CC tumours resistant to traditional chemotherapy. The present sequence  
 CC represents the extracellular region of the human LT-beta-receptor and  
 CC comprises the ligand binding domain  
 XX  
 SQ Sequence 197 AA;

Query Match 100.0%; Score 1133; DB 2; Length 197;  
 Best Local Similarity 100.0%; Pred. No. 1.2e-78;  
 Matches 197; Conservative 0; Mismatches 0; Indels 0; Gaps 0;  
 QY 1 SQQAVPPVASENOTCRDQKEYEYEPQHRICCSRCPPGTYVSACKSRIRDVTVCATCAENS 60  
 DB 1 SQQAVPPVASENOTCRDQKEYEYEPQHRICCSRCPPGTYVSACKSRIRDVTVCATCAENS 60  
 QY 61 YNEHWNLYTICQLCRPCDPVMGLEEIAPTCKRKTQCRQCPGMFCAAWALECTHCELLSD 120  
 DB 61 YNEHWNLYTICQLCRPCDPVMGLEEIAPTCKRKTQCRQCPGMFCAAWALECTHCELLSD 120  
 QY 121 CPPGTEAELKDEVGKNNHCVPCKAGHFQNTSSPSARCQPHTRCENQGLVEAAPGTAQSD 180  
 DB 121 CPPGTEAELKDEVGKNNHCVPCKAGHFQNTSSPSARCQPHTRCENQGLVEAAPGTAQSD 180  
 QY 181 TTCKNPLEPLPPEMSGT 197  
 DB 181 TTCKNPLEPLPPEMSGT 197

RESULT 3  
 ADO43009  
 ID ADO43009 standard; protein; 197 AA.  
 XX  
 AC ADO43009;  
 XX  
 DT 29-JUL-2004 (first entry)  
 DE Lymphotoxin-beta receptor (soluble form).  
 XX  
 KW Human; Lymphotoxin-beta receptor; receptor; immunomodulator;  
 KW antirheumatic; antiarthritic; antidiabetic; urologic; dermatological.  
 OS Homo sapiens.  
 XX  
 FN WO2004039329-A2.  
 XX  
 PD 13-MAY-2004.  
 XX  
 PF 31-OCT-2003; 2003WO-US034813.  
 XX  
 PR 31-OCT-2002; 2002US-0422588P.  
 XX  
 PA (BIOJ ) BIOGEN INC.  
 XX  
 PI Gommerman J, Browning JL;  
 XX  
 DR WPI; 2004-376051/35.  
 XX  
 PT Treating an animal having an immunological renal disorder or  
 PT glomerulonephritis comprises administering to the mammal a composition  
 PT comprising an inhibitor of the lymphotoxin (LT) pathway.  
 XX  
 PS Claim 7; SEQ ID NO 1; 47pp; English.

XX The present is the protein sequence of a soluble lymphotoxin-beta  
 CC receptor (LTBR) comprising the extracellular domain of LTBR that is  
 CC capable of binding lymphotoxin (LT) specifically. The invention provides  
 CC methods for treating immunological disorders, including pathologies  
 CC associated with immunoglobulin deposits in the kidneys. It is based in



CC The present invention describes human tumour necrosis factor receptor 2  
 CC related protein variant (TNFR2PV). TNFR2PV has cytotostatic, antiaethmatic  
 CC and immunosuppressive activities, and can be used in gene therapy. The  
 CC TNFR2PV cDNA or protein sequences can be used for preparing a composition  
 CC for treating a disease or condition associated with increased TNF  
 CC signalling e.g., cancer of the prostate, ovary, gallbladder, breast,  
 CC brain, liver or colon, or inflammatory disorders, such as rheumatoid  
 CC arthritis, asthma or ulcerative colitis. The present sequence represents  
 CC a human TNFR2 related protein/TNFR2beta amino acid sequence, which is given  
 CC in comparison with human TNFR2PV in the exemplification of the present  
 CC invention  
 XX

SQ Sequence 435 AA;

Query Match 100.0%; Score 1133; DB 6; Length 435;  
 Best Local Similarity 100.0%; Pred. No. 2.8e-78;  
 Matches 197; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 SQQAVPPYASENQTCDQKEYYEPOHRIICCSRCPPGTYVSACKSRIRDTVCATCAENS 60  
 DB 28 SQQAVPPYASENQTCDQKEYYEPOHRIICCSRCPPGTYVSACKSRIRDTVCATCAENS 87  
 QY 61 YNEHWNLYITICQLCRPCDPVWGLEIEIAPCTSKRKTQCRQCPGMFCAAWALECTHCELLSD 120  
 DB 88 YNEHWNLYITICQLCRPCDPVWGLEIEIAPCTSKRKTQCRQCPGMFCAAWALECTHCELLSD 147  
 QY 121 CPPGTEAELKDEVGKNNHCVPCKAGHFQNTSSPSARCQPHTRCENQGLVEAAPGTAQSD 180  
 DB 148 CPPGTEAELKDEVGKNNHCVPCKAGHFQNTSSPSARCQPHTRCENQGLVEAAPGTAQSD 207  
 QY 181 TTCKNPLEPLPPMSGT 197  
 DB 208 TTCKNPLEPLPPMSGT 224

RESULT 6  
 ABR40220  
 ID ABR40220 standard; protein; 435 AA.  
 AC ABR40220;  
 XX

12-JUN-2003 (first entry)

Human genoxin.

Human; genoxin; antiarteriosclerotic; antidiabetic; hypotensive;  
 antiinflammatory; cardiant; cerebroprotective; gene therapy;  
 tumour necrosis factor receptor; TNFR; body mass; weight loss; obesity.

Homo sapiens.

Key	Location/Qualifiers
Peptide	1..30
Protein	/label= Signal_peptide
Domain	31..435
Domain	/label= Mature_genoxin
Domain	228..248
Domain	/label= Extracellular_domain
Domain	/label= Transmembrane_domain
Domain	249..435
Domain	/label= Intracellular_domain

WO2003011322-A1.

13-FEB-2003.

31-JUL-2002; 2002WO-IB003417.

02-AUG-2001; 2001US-0309917P.

(GEST ) GENSET SA.

XX PI Lucas J, Dialynas D, Briggs K;  
 XX WPI; 2003-256417/25.  
 DR N-PSDB; ABZ99578.  
 XX Screening for an agonist or antagonist of Genoxin activity, useful for  
 PT preventing or treating metabolic disorders, comprises contacting Genoxin  
 FT polypeptide with a test compound and determining binding.  
 XX Example 10; Page 33-34; 37pp; English.  
 XX The invention relates to a novel method for screening for an agonist or  
 CC antagonist of Genoxin activity. The agonists/antagonists of the invention  
 CC have antiarteriosclerotic, antidiabetic, hypotensive, antilipaeamic,  
 CC anorectic, immunomodulator, cytostatic, anti-HIV, antiinflammatory,  
 CC cardiant, and cerebroprotective activity. The polypeptides of the  
 CC invention may have a use in gene therapy, and act as tumour necrosis  
 CC factor receptor (TNFR) agonists. The method is used to screen for an  
 CC agonist or antagonist of Genoxin. The method is useful in metabolic  
 CC research, particularly, in discovering compounds that modulate Genoxin  
 CC activity or that reduce or increase body mass and maintain weight loss,  
 CC and in preventing or treating obesity-related diseases or disorders such  
 CC as hyperlipidaemia, atherosclerosis, heart disease, stroke, insulin-  
 CC resistant diabetes or hypertension, or for preventing or treating  
 CC disorders associated with excessive weight loss, such as cachexia, cancer  
 CC -related weight loss, acquired immunodeficiency syndrome (AIDS)-related  
 CC weight loss, chronic inflammatory disease-related weight loss, or  
 CC anorexia. The present sequence represents the human genoxin of the  
 CC invention  
 XX

SQ Sequence 435 AA;

Query Match 100.0%; Score 1133; DB 6; Length 435;  
 Best Local Similarity 100.0%; Pred. No. 2.8e-78;  
 Matches 197; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 SQQAVPPYASENQTCDQKEYYEPOHRIICCSRCPPGTYVSACKSRIRDTVCATCAENS 60  
 DB 28 SQQAVPPYASENQTCDQKEYYEPOHRIICCSRCPPGTYVSACKSRIRDTVCATCAENS 87  
 QY 61 YNEHWNLYITICQLCRPCDPVWGLEIEIAPCTSKRKTQCRQCPGMFCAAWALECTHCELLSD 120  
 DB 88 YNEHWNLYITICQLCRPCDPVWGLEIEIAPCTSKRKTQCRQCPGMFCAAWALECTHCELLSD 147  
 QY 121 CPPGTEAELKDEVGKNNHCVPCKAGHFQNTSSPSARCQPHTRCENQGLVEAAPGTAQSD 180  
 DB 148 CPPGTEAELKDEVGKNNHCVPCKAGHFQNTSSPSARCQPHTRCENQGLVEAAPGTAQSD 207  
 QY 181 TTCKNPLEPLPPMSGT 197  
 DB 208 TTCKNPLEPLPPMSGT 224

RESULT 7

ABU89821  
 ID ABU89821 standard; protein; 435 AA.  
 XX

ABU89821;

10-JUL-2003 (first entry)

TNF-receptor associated factor 5 (TRAF5) interacting protein #1.

Human; cytotostatic; DAPK3-Agonist; DAPK3-Antagonist; cancer;  
 KW TNF-receptor associated factor 5 interacting protein;  
 KW tumour necrosis factor associated factor 5 interacting protein;  
 KW TRAF5 interacting protein.

Homo sapiens.

WO2003031571-A2.

XX

PD 17-APR-2003.  
 XX  
 PP 02-OCT-2002; 2002WO-US031357.  
 XX  
 XX 05-OCT-2001; 2001US-0327454P.  
 PR 09-OCT-2001; 2001US-0327917P.  
 PR 09-OCT-2001; 2001US-0328029P.  
 PR 09-OCT-2001; 2001US-0328056P.  
 PR 12-OCT-2001; 2001US-0328849P.  
 PR 15-OCT-2001; 2001US-0329414P.  
 PR 17-OCT-2001; 2001US-0330142P.  
 PR 22-OCT-2001; 2001US-0341058P.  
 PR 24-OCT-2001; 2001US-0343629P.  
 PR 29-OCT-2001; 2001US-0349575P.  
 PR 01-NOV-2001; 2001US-0346357P.  
 PR 25-JUN-2002; 2002US-0391342P.  
 PR 01-OCT-2002; 2002US-00262445.  
 XX  
 PA (CURA-) CURAGEN CORP.  
 XX  
 PI Alsobrook JR, Burgess CE, Catterton E, Chant JS, Chaudhuri A;  
 PI Binger SR, Gerlach VL, Giot L, Gorman L, Guo X, Kekuda R;  
 PI Mezes PS, Millet I, Ooi CE, Patturajan M, Rieger DK, Spytek KA;  
 PI Taupier RJ, Zerhusen BD, Zhong H, Zhong M;  
 XX  
 DR WPI; 2003-381704/36.  
 DR N-PSDB; ACA90237.  
 XX  
 XX New DAPK3 polypeptide, useful for preparing a composition for treating or  
 PT preventing e.g., cancer.  
 PT  
 XX Example 20F; Page 240; 253pp; English.  
 XX  
 CC The invention describes an isolated polypeptide comprising any of 33 90-  
 CC 1273 amino acid sequences (I) given in the specification or its mature  
 CC form, a sequence that is at least 95 % identical to (I), or a sequence  
 CC comprising one or more conservative substitutions in the amino acid  
 CC sequence of (I). The polypeptide is useful for preparing a composition  
 CC for treating or preventing e.g. cancer. This is the amino acid sequence  
 CC of a tumour necrosis factor (TNF)-receptor associated factor 5 (TRAF5)  
 CC interacting protein associated with the identification of novel human  
 CC proteins and their functions  
 XX  
 SQ Sequence 435 AA;  
 Query Match 100.0%; Score 1133; DB 6; Length 435;  
 Best Local Similarity 100.0%; Pred. No. 2.8e-78;  
 Matches 197; Conservative 0; Mismatches 0; Indels 0; Gaps 0;  
 QY 1 SQQAVPPYASENQTCDQKEYYEPQHRICCSRCPPGTYVSAKCSRIKDTVCATCAENS 60  
 DB 28 SQQAVPPYASENQTCDQKEYYEPQHRICCSRCPPGTYVSAKCSRIKDTVCATCAENS 87  
 QY 61 YNEHWNLYTICQLCRPCDPVWGLEIEIAPCTSKRKTQCRQCPGMFCAAWALECTHCELLSD 120  
 DB 88 YNEHWNLYTICQLCRPCDPVWGLEIEIAPCTSKRKTQCRQCPGMFCAAWALECTHCELLSD 147  
 QY 121 CPPGTEAEALKDEVGKGNHCVCKAGHFQNTSSPSARCOPHTRCENQGLVEAAPGTAQSD 180  
 DB 148 CPPGTEAEALKDEVGKGNHCVCKAGHFQNTSSPSARCOPHTRCENQGLVEAAPGTAQSD 207  
 QY 181 TTCKNPLEPLPPMSGT 197  
 DB 208 TTCKNPLEPLPPMSGT 224  
 RESULT 8  
 ADF50693  
 ID ADF50693 standard; protein; 435 AA.  
 XX  
 AC ADF50693;  
 XX  
 DT 12-FEB-2004 (first entry)

XX  
 DE Human lymphotoxin-beta protein.  
 XX  
 KW human; lymphotoxin-beta; allograft rejection; graft versus host disease;  
 KW Herpesvirus entry mediator; HVEM; LIGHT; immunosuppressive; cyclosporin;  
 KW corticosteroid; antiproliferative; HVEM-LIGHT inhibitor; cytokine;  
 KW TNF-family ligand; delayed hypersensitivity; atrophic gastritis;  
 KW thyroiditis; allergic encephalomyelitis; autoimmune haemolytic anaemia;  
 KW sympathetic ophthalmia; systemic lupus erythematosus;  
 KW rheumatoid arthritis; multiple sclerosis; myasthenia gravis;  
 KW immune disorder.  
 XX  
 OS Homo sapiens.  
 XX  
 PN EP1336619-A2.  
 XX  
 XX 20-AUG-2003.  
 XX  
 PF 18-FEB-2003; 2003EP-00003651.  
 XX  
 PR 19-FEB-2002; 2002US-0358463P.  
 XX  
 PA (MILL-) MILLENIUM PHARM INC.  
 XX  
 PI Fraser CC, Hancock W;  
 PI  
 XX WPI; 2003-665560/63.  
 DR N-PSDB; ADF50692.  
 XX  
 DR A composition containing an immunosuppressive agent and a molecule which  
 PT inhibits binding of Herpesvirus entry mediator to the tumor necrosis  
 PT factor superfamily member LIGHT is useful to treat or prevent immune  
 PT disorders.  
 XX  
 PS Disclosure; SEQ ID NO 17; 52pp; English.  
 XX  
 CC This invention relates to a novel method for suppressing immune disorders  
 CC such as allograft rejection or graft versus host disease. Specifically,  
 CC it comprises a Herpesvirus entry mediator (HVEM)-LIGHT inhibitor and an  
 CC immunosuppressive agent to prepare a pharmaceutical composition that can  
 CC treat or prevent an immune disorder. The present invention describes the  
 CC immunosuppressive agent as, for example, a cyclosporin, corticosteroid or  
 CC an antiproliferative agent, whereas the HVEM-LIGHT inhibitor can be an  
 CC antibody or any molecule including dominant negative proteins (such as  
 CC soluble HVEM proteins) that can disrupt binding between the cytokine  
 CC LIGHT (a TNF-family ligand also known as Tango-69, which is expressed by  
 CC activated T cells) and its receptor HVEM. As such, these compositions can  
 CC be used for the treatment of delayed hypersensitivity, atrophic  
 CC gastritis, thyroiditis, allergic encephalomyelitis, autoimmune haemolytic  
 CC anaemia, sympathetic ophthalmia, systemic lupus erythematosus, rheumatoid  
 CC arthritis, multiple sclerosis or myasthenia gravis. This polypeptide is  
 CC the human lymphotoxin-beta protein sequence, a dominant negative form of  
 CC a receptor to which LIGHT binds other than HVEM, used in an  
 CC exemplification of the invention.  
 XX  
 SQ Sequence 435 AA;  
 Query Match 100.0%; Score 1133; DB 7; Length 435;  
 Best Local Similarity 100.0%; Pred. No. 2.8e-78;  
 Matches 197; Conservative 0; Mismatches 0; Indels 0; Gaps 0;  
 QY 1 SQQAVPPYASENQTCDQKEYYEPQHRICCSRCPPGTYVSAKCSRIKDTVCATCAENS 60  
 DB 28 SQQAVPPYASENQTCDQKEYYEPQHRICCSRCPPGTYVSAKCSRIKDTVCATCAENS 87  
 QY 61 YNEHWNLYTICQLCRPCDPVWGLEIEIAPCTSKRKTQCRQCPGMFCAAWALECTHCELLSD 120  
 DB 88 YNEHWNLYTICQLCRPCDPVWGLEIEIAPCTSKRKTQCRQCPGMFCAAWALECTHCELLSD 147  
 QY 121 CPPGTEAEALKDEVGKGNHCVCKAGHFQNTSSPSARCOPHTRCENQGLVEAAPGTAQSD 180  
 DB 148 CPPGTEAEALKDEVGKGNHCVCKAGHFQNTSSPSARCOPHTRCENQGLVEAAPGTAQSD 207



ABM81345	ABM81346 standard; protein; 435 AA.	DB	88	YNEHNYLTICQLCRPCDPVWGLEETAPCTSKRKTQCRQCPGMFCAAWALECTHCELLSD	147
XX					
AC	ABM81346;	QY	121	CPPGTEAEELKDEVGKGNHCVCKAGHFONTSSPSARCPQHTRCENQGLVEAAPGTAQSD	180
XX					
XX		DB	148	CPFGTEAEELKDEVGKGNHCVCKAGHFONTSSPSARCPQHTRCENQGLVEAAPGTAQSD	207
DT	18-NOV-2004 (first entry)				
XX					
XX	Tumour-associated antigenic target (TAT) polypeptide PRO2622, SEQ:3477.	QY	181	TTCKNPLEPLPPPEMSGT 197	
DE					
XX	Tumour-associated antigenic target; TAT; human; overexpression; cancer;				
KW	tumour; diagnosis; cell proliferative disorder; breast cancer;				
KW	colorectal cancer; lung cancer; ovarian cancer; liver cancer;				
KW	central nervous system cancer; bladder cancer; pancreatic cancer;				
KW	cervical cancer; melanoma; leukaemia; hybridisation probe;				
KW	chromosome identification; chromosome mapping; gene mapping;				
KW	gene therapy; cytostatic.				
XX					
OS	Homo sapiens.				
XX					
XX	WO2004030615-A2.	FN			
XX					
XX	15-APR-2004.	PD			
XX					
XX	29-SEP-2002; 2003WO-US028547.	PF			
XX					
XX	02-OCT-2002; 2002US-041971P.	PR			
XX	(GETH ) GENENTECH INC.	PA			
XX					
XX	Wu TD, Zhang Z, Zhou Y;	PI			
XX					
XX	WPI; 2004-347921/32.	DR			
DR	N-PSDB; ACN39374.	DR			
XX					
PT	New tumor-associated antigenic target polypeptides and nucleic acids,				
PT	useful in preparing a medicament for treating or detecting a				
PT	proliferative disorder, e.g. breast, lung, colorectal, ovarian or				
PT	prostate cancer or tumor.				
XX					
PS	Claim 12; SEQ ID NO 3477; 7273pp; English.				
XX					
XX	The invention relates to human tumour-associated antigenic target (TAT)				
CC	polypeptides, and their related nucleic acids. The TAT polypeptides are				
CC	overexpressed in cancer tissues compared to normal tissues, and may thus				
CC	serve as effective targets for the diagnosis and treatment of cancer in				
CC	mammals. The invention also relates to nucleic acid and polypeptide				
CC	sequences at least 80% identical to the TAT nucleic acids and				
CC	polypeptides; expression vectors and host cells comprising a TAT nucleic				
CC	acid; an antibody specific for a TAT polypeptide; a peptide or organic				
CC	molecule which binds to a TAT polypeptide; fusion proteins comprising a				
CC	TAT polypeptide; and methods and compositions for the treatment or				
CC	diagnosis of cancer in mammals. TAT polypeptides, nucleic acids,				
CC	antibodies, antagonists, binding molecules and compositions are useful				
CC	for diagnosing or treating a cell proliferative disorder associated with				
CC	increased TAT expression, particularly cancers such as breast cancer,				
CC	colorectal cancer, lung cancer, ovarian cancer, liver cancer, bladder				
CC	cancer, pancreatic cancer, cervical cancer, cancers of the central				
CC	nervous system, melanoma and leukaemia. TAT nucleic acids may further be				
CC	used as hybridisation probes, in chromosome and gene mapping, in				
CC	chromosome identification and in gene therapy. The present sequence				
CC	represents a TAT polypeptide of the invention				
XX					
XX	Sequence 435 AA;				
QY	Query Match 100.0%; Score 1133; DB 8; Length 435;				
DB	Best Local Similarity 100.0%; Pred. No. 2.8e-78;				
XX	Matches 197; Conservative 0; Mismatches 0; Indels 0; Gaps 0;				
QY	1 SQPQAVPPVASENQTCRDEQKEYRPHQIRCCSPGPGTYYSAKCSIRDTVCATCAENS 60				
DB	28 SQPQAVPPVASENQTCRDEQKEYRPHQIRCCSPGPGTYYSAKCSIRDTVCATCAENS 87				
QY	61 YNEHNYLTICQLCRPCDPVWGLEETAPCTSKRKTQCRQCPGMFCAAWALECTHCELLSD 120				



SQ Sequence 439 AA;  
 Query Match 100.0%; Score 1133; DB 8; Length 439;  
 Best Local Similarity 100.0%; Pred. No. 2.8e-78;  
 Matches 197; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 SQQAVPPYASENQTCDQEKYEYEPQHRICCSRCPPGTYVSACKSRIRDTVCATCAENS 60  
 DB 28 SQQAVPPYASENQTCDQEKYEYEPQHRICCSRCPPGTYVSACKSRIRDTVCATCAENS 87

QY 61 YNEHWNLYTICQLCRPCDPVWGLEIEIAPCTSKRKTQCRQCPGMFCAAWALECTHCELLSD 120  
 DB 88 YNEHWNLYTICQLCRPCDPVWGLEIEIAPCTSKRKTQCRQCPGMFCAAWALECTHCELLSD 147

QY 121 CPPGTAEALKDEVGKNNHCVPCKAGHFQNTSSPSARCQPHTRCENQGLVEAAPGTAQSD 180  
 DB 148 CPPGTAEALKDEVGKNNHCVPCKAGHFQNTSSPSARCQPHTRCENQGLVEAAPGTAQSD 207

QY 181 TTCKNPLEPLPPMSGT 197  
 DB 208 TTCKNPLEPLPPMSGT 224

RESULT 13  
 ABM83610  
 ID ABM83610 standard; protein; 446 AA.  
 AC ABM83610;  
 XX  
 DT 18-NOV-2004 (first entry)  
 DE Human diagnostic and therapeutic pprotein SEQ ID NO:3859.  
 XX Gene therapy; human diagnostic and therapeutic polynucleotide; dithp.  
 KW Homo sapiens.  
 OS  
 XX WO2004023973-A2.  
 XX  
 PD 25-MAR-2004.  
 XX  
 PF 12-SEP-2003; 2003WO-US028227.  
 PR 12-SEP-2002; 2002US-0410259P.  
 PR 12-SEP-2002; 2002US-0410260P.  
 XX (INCY-) INCYTE CORP.  
 PA  
 XX Schmidt JP, Wright RJ, Bruns CM, Marjanovic MM, Shen F;  
 PI Harthshorne TA, Suchorolski MT, Altus CM, Pitts SJ, Elder LV;  
 PI Mooney EM, Delegeane AM, Panssar IS, Banville SC, Reddy TP;  
 PI Stevens KA, Blanchard JL, Panzer SR, Wang X, Au AP, Gerstin EH;  
 PI Peralta CH, Anderson SB, Rioux P, Shen EJ, Wu MC, Stuve LL;  
 PI Lagace RE, Spiro PA, Stewart EA, Wingrove J, Vitt UA, Kirton ES;  
 PI Xu Y, Kwong M, Policky JL, Hurwitz BL, Ma Y, Jackson JL, Gietzen D;  
 PI Patursky S, Shi X, Suarez CJ;  
 XX WPI; 2004-329368/30.  
 DR N-PSDB; ACN42262.  
 XX  
 XX New diagnostic and therapeutic polynucleotides and polypeptides, useful  
 PT in diagnosing a condition, disease or disorder associated with human  
 PT molecules, e.g. autoimmune or inflammatory disorders, in gene therapy or  
 PT in gene mapping.  
 XX  
 PS Claim 27; Page; 190pp; English.  
 XX  
 XX The invention relates to novel diagnostic and therapeutic polynucleotides  
 CC selected from one of the 2722 sequences defined in the specification. A  
 CC polynucleotide of the invention may have a use in gene therapy. The human  
 CC diagnostic and therapeutic polynucleotides (dithp) or polypeptides may be  
 CC used to diagnose a particular condition, disease or disorder associated  
 CC with human molecules, e.g. cell proliferative disorders,

CC autoimmune/inflammatory disorder, developmental disorder, endocrine  
 CC disorder, neurological disorders, gastrointestinal disorders, or  
 CC infections caused by virus, bacteria, fungi or parasite. The dithp  
 CC molecules may also be used in genetic mapping, in identifying individuals  
 CC from minute biological samples, in detecting single nucleotide  
 CC polymorphisms, as molecular weight markers, and for somatic or germline  
 CC gene therapy. The present sequence represents a dithp protein of the  
 CC invention. Note: The sequence data for this patent is not represented in  
 CC the printed specification, but was obtained in electronic format directly  
 CC from WIPO at www.wipo.int/pct/en/sequences/listing.htm  
 XX  
 SQ Sequence 446 AA;  
 Query Match 100.0%; Score 1133; DB 8; Length 446;  
 Best Local Similarity 100.0%; Pred. No. 2.8e-78;  
 Matches 197; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 SQQAVPPYASENQTCDQEKYEYEPQHRICCSRCPPGTYVSACKSRIRDTVCATCAENS 60  
 DB 28 SQQAVPPYASENQTCDQEKYEYEPQHRICCSRCPPGTYVSACKSRIRDTVCATCAENS 87

QY 61 YNEHWNLYTICQLCRPCDPVWGLEIEIAPCTSKRKTQCRQCPGMFCAAWALECTHCELLSD 120  
 DB 88 YNEHWNLYTICQLCRPCDPVWGLEIEIAPCTSKRKTQCRQCPGMFCAAWALECTHCELLSD 147

QY 121 CPPGTAEALKDEVGKNNHCVPCKAGHFQNTSSPSARCQPHTRCENQGLVEAAPGTAQSD 180  
 DB 148 CPPGTAEALKDEVGKNNHCVPCKAGHFQNTSSPSARCQPHTRCENQGLVEAAPGTAQSD 207

QY 181 TTCKNPLEPLPPMSGT 197  
 DB 208 TTCKNPLEPLPPMSGT 224

RESULT 14  
 ADJ67640  
 ID ADJ67640 standard; protein; 450 AA.  
 XX  
 AC ADJ67640;  
 XX  
 DT 06-MAY-2004 (first entry)  
 XX Human ovarian specific polypeptide SEQ ID NO:354.  
 DE human; ovarian; cytostatic; immunostimulant; vaccine; gene therapy;  
 XX human; ovarian; cytostatic; immunostimulant; vaccine; gene therapy;  
 KW ovarian cancer; immune response; cancer.  
 XX  
 OS Homo sapiens.  
 XX  
 XX WO2004013311-A2.  
 XX  
 PD 12-FEB-2004.  
 XX  
 PF 06-AUG-2003; 2003WO-US024669.  
 XX  
 PR 06-AUG-2002; 2002US-0401469P.  
 XX  
 XX (DIAD-) DIADEXUS INC.  
 PA  
 XX Macina RA, Salceda S, Liu C, Sun Y, Turner LR;  
 PI WPI; 2004-169331/16.  
 DR  
 XX New ovarian specific nucleic acid, useful in identifying, diagnosing,  
 PT monitoring, staging, imaging and treating ovarian cancer and non-  
 PT cancerous disease states in ovarian tissue.  
 XX  
 PS Claim 12; SEQ ID NO 354; 586pp; English.  
 XX  
 XX The invention relates to novel isolated ovarian specific nucleic acid  
 CC molecules and the polypeptides encoded by them. A protein of the  
 CC invention has cytostatic and immunostimulant activity. A nucleic acid  
 CC the invention may have a use as a vaccine, and in gene therapy. The



CC nucleic acid molecule or polypeptide, antibody or kit is useful in  
CC identifying, diagnosing, monitoring, staging, imaging and treating  
CC ovarian cancer and non cancerous disease states in ovarian tissue and  
CC inducing an immune response against the ovarian cancer cell. The  
CC sequences shown in ADJ67535-ADJ67682 represent ovarian specific  
CC polypeptides of the invention.  
XX  
SQ Sequence 450 AA;

Query Match 100.0%; Score 1133; DB 8; Length 450;  
Best Local Similarity 100.0%; Pred. No. 2.9e-78;  
Matches 197; Conservative 0; Mismatches 0; Indels 0; Gaps 0;  
Qy 1 SQQAVPPYASENQTCRDQEKYEPQHRICCSRCPPGTYVSACSRIRDTVCATCAENS 60  
Db 28 SQQAVPPYASENQTCRDQEKYEPQHRICCSRCPPGTYVSACSRIRDTVCATCAENS 87  
Qy 61 YNEHWNLYTICLCRCPDPMGLEEIAPTCKTKTCRCQCPGMFCAAALECTHCELLSD 120  
Db 88 YNEHWNLYTICLCRCPDPMGLEEIAPTCKTKTCRCQCPGMFCAAALECTHCELLSD 147  
Qy 121 CPPGTEAELKDEVGKGNHCVPCKAGHFONTSSPSARCQPHTRCENQGLVEAAPGTAQSD 180  
Db 148 CPPGTEAELKDEVGKGNHCVPCKAGHFONTSSPSARCQPHTRCENQGLVEAAPGTAQSD 207  
Qy 181 TTCKNPLEPLPPEMSGT 197  
Db 208 TTCKNPLEPLPPEMSGT 224

RESULT 15  
ABP96136  
ID ABP96136 standard; protein; 399 AA.  
XX AC ABP96136;

XX DT 09-MAY-2003 (first entry)  
XX DE Human TNF receptor 2 related protein variant SEQ ID NO:1.

XX KW Human; tumour necrosis factor receptor 2 related protein variant;  
XX TNFR2PV; cystostatic; immunosuppressive; antiasthmatic; gene therapy;  
XX TNF signalling; cancer; inflammatory disorder; rheumatoid arthritis;  
XX asthma; ulcerative colitis.

XX OS Homo sapiens.

XX PN WO2003012037-A2.

XX PD 13-FEB-2003.

XX PF 24-JUL-2002; 2002WO-US023684.

XX PR 27-JUL-2001; 2001US-00917372.

XX PA (INCY-) INCYTE GENOMICS INC.

XX PI Lal PG, Warren BA;

XX WPI; 2003-256445/25.

XX DR N-PSDB; AB279717.

XX PT New cDNA, useful for preparing a composition for treating a disease or  
XX condition associated with increased TNF signaling e.g., cancer of the  
XX prostate, ovary, gallbladder, breast, brain, liver or colon, or  
XX PT rheumatoid arthritis, asthma.

XX PS Claim 20; Fig 1A-F; 64pp; English.

XX CC The present sequence represents human tumour necrosis factor receptor 2  
XX related protein variant (TNFR2PV). TNFR2PV has cystostatic, antiasthmatic  
XX and immunosuppressive activities, and can be used in gene therapy. The  
XX TNFR2PV cDNA or protein sequences can be used for preparing a composition

CC for treating a disease or condition associated with increased TNF  
CC signalling e.g., cancer of the prostate, ovary, gallbladder, breast,  
CC brain, liver or colon, or inflammatory disorders, such as rheumatoid  
CC arthritis, asthma or ulcerative colitis  
XX  
SQ Sequence 399 AA;

Query Match 99.6%; Score 1129; DB 6; Length 399;  
Best Local Similarity 99.5%; Pred. No. 5.1e-78;  
Matches 196; Conservative 1; Mismatches 0; Indels 0; Gaps 0;  
Qy 1 SQQAVPPYASENQTCRDQEKYEPQHRICCSRCPPGTYVSACSRIRDTVCATCAENS 60  
Db 28 SQQAVPPYASENQTCRDQEKYEPQHRICCSRCPPGTYVSACSRIRDTVCATCAENS 87  
Qy 61 YNEHWNLYTICLCRCPDPMGLEEIAPTCKTKTCRCQCPGMFCAAALECTHCELLSD 120  
Db 88 YNEHWNLYTICLCRCPDPMGLEEIAPTCKTKTCRCQCPGMFCAAALECTHCELLSD 147  
Qy 121 CPPGTEAELKDEVGKGNHCVPCKAGHFONTSSPSARCQPHTRCENQGLVEAAPGTAQSD 180  
Db 148 CPPGTEAELKDEVGKGNHCVPCKAGHFONTSSPSARCQPHTRCENQGLVEAAPGTAQSD 207  
Qy 181 TTCKNPLEPLPPEMSGT 197  
Db 208 TTCKNPLEPLPPEMSGS 224

Search completed: September 23, 2005, 10:27:33  
Job time : 75 secs

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GenCore version 5.1.6  
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OM protein - protein search, using sw model

Run on: September 23, 2005, 09:52:51 ; Search time 43 Seconds  
(without alignments)  
341.997 Million cell updates/sec

Title: US-10-077-406-1  
Perfect score: 1133  
Sequence: 1 SQQAVPPYASENQTCRDOE.....QSDTCKNPLELPPEMSGT 197

Scoring table: BLOSUM62

Gapop 10.0 , Gapext 0.5

Searched: 513545 seqs, 74649064 residues

Total number of hits satisfying chosen parameters: 513545

Minimum DB seq length: 0  
Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%  
Maximum Match 100%  
Listing first 45 summaries

Database : Issued Patents AA: \*  
1: /cgn2\_6/ptodata/1/iaa/5A COMB.pdp.\*  
2: /cgn2\_6/ptodata/1/iaa/5B COMB.pdp.\*  
3: /cgn2\_6/ptodata/1/iaa/6A COMB.pdp.\*  
4: /cgn2\_6/ptodata/1/iaa/6B COMB.pdp.\*  
5: /cgn2\_6/ptodata/1/iaa/PTUS COMB.pdp.\*  
6: /cgn2\_6/ptodata/1/iaa/backfile1.pdp.\*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	ID	Description
1	1133	100.0	197	2	US-08-505-606-1
2	1133	100.0	197	4	US-09-000-166-1
3	1133	100.0	197	4	US-09-303-262-1
4	1133	100.0	473	4	US-09-949-016-7944
5	987	87.1	170	4	US-08-828-683A-14
6	981	86.6	170	4	US-09-523-323-57
7	771	68.0	415	3	US-09-006-353A-6
8	771	68.0	415	4	US-09-573-986-6
9	456	40.2	77	3	US-08-866-545-3
10	456	40.2	77	3	US-09-627-775-3
11	305	26.9	227	3	US-08-974-022-48
12	305	26.9	227	3	US-08-795-445A-48
13	305	26.9	227	3	US-08-795-447A-48
14	305	26.9	227	3	US-08-974-186-48
15	305	26.9	227	3	US-08-795-446B-48
16	305	26.9	227	3	US-08-706-945D-134
17	305	26.9	227	4	US-08-577-788C-48
18	305	26.9	235	3	US-09-326-394-4
19	305	26.9	235	4	US-09-580-235-2
20	305	26.9	235	4	US-09-580-235-8
21	305	26.9	235	4	US-09-580-181-2
22	305	26.9	235	4	US-09-580-181-8
23	305	26.9	235	4	US-09-102-530-2
24	305	26.9	235	4	US-09-102-530-8
25	305	26.9	237	4	US-09-579-845-10
26	305	26.9	461	1	US-08-385-229-2
27	305	26.9	461	2	US-08-650-000-2

28	305	26.9	461	3	US-09-042-785A-7
29	305	26.9	461	3	US-08-477-347-3
30	305	26.9	461	3	US-09-006-353A-4
31	305	26.9	461	3	US-08-476-862-2
32	305	26.9	461	4	US-09-573-986-4
33	305	26.9	461	4	US-08-406-824A-2
34	305	26.9	461	4	US-09-800-909-2
35	305	26.9	461	4	US-09-758-124-2
36	305	26.9	461	4	US-09-800-908-3
37	305	26.9	461	4	US-09-896-096A-17
38	305	26.9	461	4	US-09-949-016-6019
39	305	26.9	461	6	5395760-2
40	305	26.9	461	6	5395760-2
41	305	26.9	486	1	US-08-243-010-1
42	305	26.9	491	4	US-09-949-016-7840
43	305	26.9	518	1	US-08-385-229-4
44	305	26.9	518	4	US-09-579-845-1
45	305	26.9	518	4	US-09-579-845-3

ALIGNMENTS

RESULT 1  
US-08-505-606-1  
; Sequence 1, Application US/08505606  
; Patent No. 5925351  
; GENERAL INFORMATION:  
; APPLICANT: BROWNING, Jeffrey L.  
; APPLICANT: BENJAMIN, Christopher D.  
; APPLICANT: HOCHMAN, Paula S.  
; TITLE OF INVENTION: SOLUBLE LYMPHOTOXIN-BETA RECEPTORS AND  
; TITLE OF INVENTION: ANTI-LYMPHOTOXIN RECEPTOR AND LIGAND ANTIBODIES AS  
; TITLE OF INVENTION: THERAPEUTIC AGENTS FOR THE TREATMENT OF IMMUNOLOGICAL  
; TITLE OF INVENTION: DISEASE  
; NUMBER OF SEQUENCES: 1  
; CORRESPONDENCE ADDRESS:  
; ADDRESSEE: James F. Haley, Jr.  
; STREET: 1251 Avenue of the Americas  
; CITY: New York  
; STATE: New York  
; COUNTRY: U.S.A.  
; ZIP: 10020  
; COMPUTER READABLE FORM:  
; MEDIUM TYPE: Floppy disk  
; OPERATING SYSTEM: IBM PC compatible  
; SOFTWARE: Patent In Release #1.0, Version #1.30  
; CURRENT APPLICATION DATA:  
; APPLICATION NUMBER: US/08/505,606  
; FILING DATE: 21-JUL-1995  
; CLASSIFICATION: 424  
; PRIOR APPLICATION DATA:  
; APPLICATION NUMBER: US 08/378,968  
; FILING DATE: 26-JAN-1995  
; ATTORNEY/AGENT INFORMATION:  
; NAME: HALEY, Jr., James F.  
; REGISTRATION NUMBER: 27,794  
; REFERENCE/DOCKET NUMBER: B191  
; TELECOMMUNICATION INFORMATION:  
; TELEPHONE: (212) 596-9000  
; TELEFAX: (212) 596-9090  
; TELEX: 14-8367  
; INFORMATION FOR SEQ ID NO: 1:  
; SEQUENCE CHARACTERISTICS:  
; LENGTH: 197 amino acids  
; TYPE: amino acid  
; STRANDEDNESS:  
; TOPOLOGY: linear  
; MOLECULE TYPE: peptide  
US-08-505-606-1

Query Match 100.0%; Score 1133; DB 2; Length 197;



; CURRENT FILING DATE: 2000-04-14
; PRIOR APPLICATION NUMBER: 60/241,755
; PRIOR FILING DATE: 2000-10-20
; PRIOR APPLICATION NUMBER: 60/237,768
; PRIOR FILING DATE: 2000-10-03
; PRIOR APPLICATION NUMBER: 60/231,498
; PRIOR FILING DATE: 2000-09-08
; NUMBER OF SEQ ID NOS: 207012
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO: 7944
; LENGTH: 473
; TYPE: PRT
; ORGANISM: Human
US-09-949-016-7944

Query Match 100.0%; Score 1133; DB 4; Length 473;
Best Local Similarity 100.0%; Pred. No. 9e-99; 0; Indels 0; Gaps 0;
Matches 197; Conservative 0; Mismatches 0;

QY 1 SQPQAVPPYASENQTCDQEKYYEPQHRICCSRCPPGTYVSAKCSIRIDTVCATCAENS 60
DB 66 SQPQAVPPYASENQTCDQEKYYEPQHRICCSRCPPGTYVSAKCSIRIDTVCATCAENS 125
QY 61 YNEHWNLYTICQLCRPCDPVGMGLEETAPCTSKRKTQCRCPGMFCAAWALECTHCELLSD 120
DB 126 YNEHWNLYTICQLCRPCDPVGMGLEETAPCTSKRKTQCRCPGMFCAAWALECTHCELLSD 185
QY 121 CPPTGAELKDEVGKNNHCVCCKAGHFONTSSPSARCPHTRCENQGLVEAAPGTAQSD 180
DB 186 CPPTGAELKDEVGKNNHCVCCKAGHFONTSSPSARCPHTRCENQGLVEAAPGTAQSD 245
QY 181 TTCKNPLEPLPPMSGT 197
DB 246 TTCKNPLEPLPPMSGT 262

RESULT 5
US-08-828-683A-14
; Sequence 14, Application US/08828683A
; Patent No. 6469144
; GENERAL INFORMATION:
; APPLICANT: Ashkenazi, Avi J.
; TITLE OF INVENTION: Apo-2 LI AND Apo-3 POLYPEPTIDES
; NUMBER OF SEQUENCES: 28
; CORRESPONDENCE ADDRESS:
; ADDRESSER: Genentech, Inc.
; STREET: 1 DNA Way
; CITY: South San Francisco
; STATE: California
; COUNTRY: USA
; ZIP: 94080
; COMPUTER READABLE FORM:
; MEDIUM TYPE: 3.5 inch, 1.44 Mb floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: Winpatin (Genentech)
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/828,683A
; FILING DATE: 31-Mar-1997
; CLASSIFICATION: <Unknown>
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: 08/625328
; FILING DATE: 1-Apr-1996
; APPLICATION NUMBER: 08/710802
; FILING DATE: 23-Sep-1996
; ATTORNEY/AGENT INFORMATION:
; NAME: Marechang, Diane L.
; REGISTRATION NUMBER: 35,600
; REFERENCE/DOCKET NUMBER: P1007P1
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: 650/225-5416
; TELEFAX: 650/952-9881
; INFORMATION FOR SEQ ID NO: 14:

; SEQUENCE CHARACTERISTICS:
; LENGTH: 170 amino acids
; TYPE: Amino Acid
; TOPOLOGY: Linear
; SEQUENCE DESCRIPTION: SEQ ID NO: 14:
US-08-828-683A-14
Query Match 87.1%; Score 987; DB 4; Length 170;
Best Local Similarity 100.0%; Pred. No. 1.6e-85;
Matches 170; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
QY 15 TCRDQEKYYEPQHRICCSRCPPGTYVSAKCSIRIDTVCATCAENSYNEHWNLYTICQLC 74
DB 1 TCRDQEKYYEPQHRICCSRCPPGTYVSAKCSIRIDTVCATCAENSYNEHWNLYTICQLC 60
QY 75 RCPDQVGMGLEETAPCTSKRKTQCRCPGMFCAAWALECTHCELLSDCPPTGAELKDEVG 134
DB 61 RCPDQVGMGLEETAPCTSKRKTQCRCPGMFCAAWALECTHCELLSDCPPTGAELKDEVG 120
QY 135 KGNHCVCKAGHFONTSSPSARCPHTRCENQGLVEAAPGTAQSDTTCK 184
DB 121 KGNHCVCKAGHFONTSSPSARCPHTRCENQGLVEAAPGTAQSDTTCK 170

RESULT 6
US-09-523-323-57
; Sequence 57, Application US/09523323
; Patent No. 6635743
; GENERAL INFORMATION:
; APPLICANT: Ebner, Reinhard
; APPLICANT: Yu, Guo-Liang
; APPLICANT: Ruben, Steven M.
; APPLICANT: Ullrich, Stephen
; APPLICANT: Zhai, Yifan
; TITLE OF INVENTION: Apoptosis Inducing Molecule II and Methods of Use
; FILE REFERENCE: 1488.065000C
; CURRENT APPLICATION NUMBER: US/09/523,323
; EARLIER FILING DATE: 2000-03-10
; EARLIER APPLICATION NUMBER: 60/168,380
; EARLIER FILING DATE: 1999-12-02
; EARLIER APPLICATION NUMBER: 60/148,326
; EARLIER FILING DATE: 1999-08-11
; EARLIER APPLICATION NUMBER: 60/142,657
; EARLIER FILING DATE: 1999-07-06
; EARLIER APPLICATION NUMBER: 60/137,457
; EARLIER FILING DATE: 1999-06-04
; EARLIER APPLICATION NUMBER: 60/124,041
; EARLIER FILING DATE: 1999-03-11
; EARLIER APPLICATION NUMBER: 09/252,656
; EARLIER FILING DATE: 1999-02-19
; EARLIER APPLICATION NUMBER: 60/075,409
; EARLIER FILING DATE: 1998-02-20
; EARLIER APPLICATION NUMBER: 09/027,287
; EARLIER FILING DATE: 1998-02-20
; EARLIER APPLICATION NUMBER: 09/003,886
; EARLIER FILING DATE: 1998-01-07
; EARLIER APPLICATION NUMBER: 08/822,953
; EARLIER FILING DATE: 1997-03-21
; EARLIER APPLICATION NUMBER: 60/013,923
; EARLIER FILING DATE: 1996-03-22
; EARLIER APPLICATION NUMBER: 60/030,157
; EARLIER FILING DATE: 1996-10-31
; NUMBER OF SEQ ID NOS: 70
; SOFTWARE: PatentIn Ver. 2.0
; SEQ ID NO 57
; LENGTH: 170
; TYPE: PRT
; ORGANISM: Homo sapiens
; FEATURE:
; NAME/KEY: UNSURE
; LOCATION: (7)
; OTHER INFORMATION: May be any amino acid
US-09-523-323-57

Query Match 86.6%; Score 981; DB 4; Length 170;  
Best Local Similarity 99.4%; Pred. No. 6e-85;  
Matches 169; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 15 TCRDQKEYEYPOHRIICSCPCPGTIVSAKCSRIKRTVCAATCAENSYNEHWNLYTICOLC 74  
DB 1 TCRDQKEYEYPOHRIICSCPCPGTIVSAKCSRIKRTVCAATCAENSYNEHWNLYTICOLC 60  
QY 75 RCPDVPVGLBEIAPICTSKRTQCRQCPGMFCAWALECTHCELLSDCPPGTEAELKDEVG 134  
DB 61 RCPDVPVGLBEIAPICTSKRTQCRQCPGMFCAWALECTHCELLSDCPPGTEAELKDEVG 120  
QY 135 KGNHCVCKAGHFQNTSSPSCARCPHTRCENQGLVEAAPGTAQSDTTCK 184  
DB 121 KGNHCVCKAGHFQNTSSPSCARCPHTRCENQGLVEAAPGTAQSDTTCK 170

## RESULT 7

US-09-006-353A-6

; Sequence 6, Application US/09006353A

; Patent No. 6261801

; GENERAL INFORMATION:

; APPLICANT: WEI, YING-FEI

; APPLICANT: YU, GUO-LIANG

; APPLICANT: GENTZ, REINER

; APPLICANT: RUBEN, STEVEN

; TITLE OF INVENTION: TUMOR NECROSIS FACTOR RECEPTOR 5

; NUMBER OF SEQUENCES: 26

; CORRESPONDENCE ADDRESS:

; ADDRESSEE: HUMAN GENOME SCIENCES, INC.

; STREET: 9410 KEY WEST AVENUE

; CITY: ROCKVILLE

; STATE: MD

; COUNTRY: US

; ZIP: 20850

; COMPUTER READABLE FORM:

; MEDIUM TYPE: Floppy disk

; COMPUTER: IBM PC compatible

; OPERATING SYSTEM: PC-DOS/MS-DOS

; SOFTWARE: PatentIn Release #1.0, Version #1.30

; CURRENT APPLICATION DATA:

; APPLICATION NUMBER: US/09/006,353A

; FILING DATE:

; CLASSIFICATION: 435

; ATTORNEY/AGENT INFORMATION:

; NAME: BROOKES, ANDERS A

; REGISTRATION NUMBER: 36,373

; REFERENCE/DOCKET NUMBER: PF341

; TELECOMMUNICATION INFORMATION:

; TELEPHONE: (301) 309-8504

; TELEFAX: (301) 309-8512

; INFORMATION FOR SEQ ID NO: 6:

; SEQUENCE CHARACTERISTICS:

; LENGTH: 415 amino acids

; TYPE: amino acid

; STRANDEDNESS: single

; TOPOLOGY: linear

; MOLECULE TYPE: protein

; US-09-006-353A-6

Query Match 86.0%; Score 771; DB 3; Length 415;  
Best Local Similarity 70.7%; Pred. No. 9.7e-65;  
Matches 135; Conservative 14; Mismatches 40; Indels 2; Gaps 1;

QY 1 SQQAVPPVASENOTCRDQKEYEYPOHRIICSCPCPGTIVSAKCSRIKRTVCAATCAENS 60  
DB 28 SQQAVPPVASENOTCRDQKEYEYPOHRIICSCPCPGTIVSAKCSRIKRTVCAATCAENS 87  
QY 61 YNEHWNLYTICQLCRPCDPVGMLEIEIAPCTSKRTQCRQCPGMFCAWALECTHC--ELL 118  
DB 88 YNEHWNHLSLTCQLCRPCDIVLGFEVAPCTSDRKAECRCQPGMSCVYLDNECVHCEERL 147

QY 119 SDCPGETAELKDEYKGNHCVCKAGHFQNTSSPSCARCPHTRCENQGLVEAAPGTAQ 178  
DB 148 VLCQFGTEAEVYDEIMDTDVNCVPCPKPGHFQNTSSPSCARCPHTRCETIQGLVEAAPGTSY 207  
QY 179 SDTICKNPLEP 189  
DB 208 SDTICKNPPPEP 218

## RESULT 8

US-09-573-986-6

; Sequence 6, Application US/09573986

; Patent No. 6455040

; GENERAL INFORMATION:

; APPLICANT: Wei, Ying-Fei

; APPLICANT: Ni, Jian

; APPLICANT: Gentz, Reiner

; APPLICANT: Ruben, Steven

; TITLE OF INVENTION: Tumor Necrosis Factor Receptor 5

; FILE REFERENCE: 1488.1280004

; CURRENT APPLICATION NUMBER: US/09/573,986

; CURRENT FILING DATE: 2000-05-18

; NUMBER OF SEQ ID NOS: 27

; SOFTWARE: PatentIn Ver. 2.1

; SEQ ID NO 6

; LENGTH: 415

; TYPE: PRT

; ORGANISM: Homo sapiens

; US-09-573-986-6

Query Match 68.0%; Score 771; DB 4; Length 415;  
Best Local Similarity 70.7%; Pred. No. 9.7e-65;  
Matches 135; Conservative 14; Mismatches 40; Indels 2; Gaps 1;

QY 1 SQQAVPPVASENOTCRDQKEYEYPOHRIICSCPCPGTIVSAKCSRIKRTVCAATCAENS 60  
DB 28 SQQAVPPVASENOTCRDQKEYEYPOHRIICSCPCPGTIVSAKCSRIKRTVCAATCAENS 87  
QY 61 YNEHWNLYTICQLCRPCDPVGMLEIEIAPCTSKRTQCRQCPGMFCAWALECTHC--ELL 118  
DB 88 YNEHWNHLSLTCQLCRPCDIVLGFEVAPCTSDRKAECRCQPGMSCVYLDNECVHCEERL 147  
QY 119 SDCPGETAELKDEYKGNHCVCKAGHFQNTSSPSCARCPHTRCENQGLVEAAPGTAQ 178  
DB 148 VLCQFGTEAEVYDEIMDTDVNCVPCPKPGHFQNTSSPSCARCPHTRCETIQGLVEAAPGTSY 207  
QY 179 SDTICKNPLEP 189  
DB 208 SDTICKNPPPEP 218

## RESULT 9

US-08-866-545-3

; Sequence 3, Application US/08866545

; Patent No. 6265535

; GENERAL INFORMATION:

; APPLICANT: Greene, Mark I.

; APPLICANT: Murali, Ramachandran

; APPLICANT: Takasaki, Wataru

; TITLE OF INVENTION: PEPTIDES AND PEPTIDE

; TITLE OF INVENTION: ANALOGUES DESIGNED FROM BINDING SITES OF TUMOR

; TITLE OF INVENTION: NECROSIS FACTOR RECEPTOR SUPERFAMILY AND THEIR

; NUMBER OF SEQUENCES: 27

; CORRESPONDENCE ADDRESS:

; ADDRESSEE: pennie &amp; Edmonds LLP

; STREET: 1155 Avenue of the Americas

; CITY: New York

; STATE: NY

; COUNTRY: USA

; ZIP: 10036-2811

; COMPUTER READABLE FORM:

; MEDIUM TYPE: Diskette

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; COMPUTER: IBM Compatible
; OPERATING SYSTEM: DOS
; SOFTWARE: FastSeq Version 2.0
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/866,545
; FILING DATE: 30-MAY-1997
; CLASSIFICATION: 530
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER:
; FILING DATE:
; ATTORNEY/AGENT INFORMATION:
; NAME: Coruzzi, Laura A.
; REGISTRATION NUMBER: 30,742
; REFERENCE/DOCKET NUMBER: 009113-0004-999
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: 650-493-4935
; TELEFAX: 650-493-5556
; TELEX: 66141 PENNIE
; INFORMATION FOR SEQ ID NO: 3:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 77 amino acids
; TYPE: amino acid
; STRANDEDNESS: single
; TOPOLOGY: linear
; MOLECULE TYPE: No. 6265535e
; US-08-866-545-3

Query Match 40.2%; Score 456; DB 3; Length 77;
Best Local Similarity 100.0%; Pred. No. 7e-36; 0; Indels 0; Gaps 0;
Matches 77; Conservative 0; Mismatches 0;

; QY 52 VCATCAENSYNEHWNLTICQLCRPCDPVWGLEEIAICTSKRKTQRCQPGMFCFAAWALE 111
; Db 1 VCATCAENSYNEHWNLTICQLCRPCDPVWGLEEIAICTSKRKTQRCQPGMFCFAAWALE 60

; QY 112 CTHCELLSDCPPGTAE 128
; Db 61 CTHCELLSDCPPGTAE 77

RESULT 10
US-09-627-775-3
; Sequence 3, Application US/09627775
; Patent No. 6682739
; GENERAL INFORMATION:
; APPLICANT: Greene, Mark
; APPLICANT: Murali, Ramachandran
; APPLICANT: Aoki, Kazuhiko
; APPLICANT: Baron, Roland
; TITLE OF INVENTION: Methods of Inhibiting Osteoclastogenesis
; FILE REFERENCE: UPN3832
; CURRENT APPLICATION NUMBER: US/09/627,775
; CURRENT FILING DATE: 2000-07-28
; PRIOR APPLICATION NUMBER: 60/146,090
; PRIOR FILING DATE: 1999-07-28
; NUMBER OF SEQ ID NOS: 29
; SOFTWARE: PatentIn Ver. 2.1
; SEQ ID NO 3
; LENGTH: 77
; TYPE: PRT
; ORGANISM: Homo sapiens
; US-09-627-775-3

Query Match 40.2%; Score 456; DB 4; Length 77;
Best Local Similarity 100.0%; Pred. No. 7e-36; 0; Indels 0; Gaps 0;
Matches 77; Conservative 0; Mismatches 0;

; QY 52 VCATCAENSYNEHWNLTICQLCRPCDPVWGLEEIAICTSKRKTQRCQPGMFCFAAWALE 111
; Db 1 VCATCAENSYNEHWNLTICQLCRPCDPVWGLEEIAICTSKRKTQRCQPGMFCFAAWALE 60

; QY 112 CTHCELLSDCPPGTAE 128
; Db 112 CTHCELLSDCPPGTAE 128
```

```
Db 61 CTHCELLSDCPPGTAE 77

RESULT 11
US-08-974-022-48
; Sequence 48, Application US/08974022
; Patent No. 6015938
; GENERAL INFORMATION:
; APPLICANT: Boyle, William J.
; APPLICANT: Lacey, David L.
; APPLICANT: Calzone, Frank J.
; APPLICANT: Chang, Ming-Shi
; TITLE OF INVENTION: OSTEOPROTEGERIN
; NUMBER OF SEQUENCES: 53
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Amgen Inc.
; STREET: 1840 Behavilland Drive
; CITY: Thousand Oaks
; STATE: California
; COUNTRY: USA
; ZIP: 91320-1789
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC Compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: PatentIn Release #1.0, Version #1.30
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/974,022
; FILING DATE: 12-DEC-1995
; CLASSIFICATION:
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: 08/577,788
; FILING DATE:
; ATTORNEY/AGENT INFORMATION:
; NAME: Winter, Robert B.
; REFERENCE/DOCKET NUMBER: A-378
; INFORMATION FOR SEQ ID NO: 48:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 227 amino acids
; TYPE: amino acid
; STRANDEDNESS: single
; TOPOLOGY: linear
; MOLECULE TYPE: protein
; US-08-974-022-48

Query Match 26.9%; Score 305; DB 3; Length 227;
Best Local Similarity 35.0%; Pred. No. 3.9e-21;
Matches 70; Conservative 24; Mismatches 78; Indels 28; Gaps 9;

; QY 5 AVPPYASE-NOTCRDQEKEYEPQHRICCSRCPPGTYVSAKCSRIKDTVCATCAENSYNE 63
; Db 28 APTPYAPERGSTCR--LREYDQTAQMCCKSCSPQHAKVFCTKTSKTDVCDSCEDSTYIQ 85
; QY 64 HNNYLTICQLCR---PCDPVWGLEEIAICTSKRKTQRCQPGMFCFAAWALE--CTHCELLS 119
; Db 86 LNNWPECLSCGSRCSQV----ETQACTREQNRICITCRPGWYCALSKQEGRCILCAPLR 141
; QY 120 DCPPG-----TEALKDEVGKNNHCVPCKAGHFONTSSPSARCCOPHTRCENQGLVEAP 174
; Db 142 KCRPGFGVARPGTETSDVW-----CKPCAPGTFSTNTSSDTCRPHQICN-----VVAIP 191
; QY 175 GTAQSDTTTC--KNPLEPLPP 192
; Db 192 GNASRDVACTSTSPTRSNAP 211

RESULT 12
US-08-795-445A-48
; Sequence 48, Application US/08795445A
; Patent No. 6284485
; GENERAL INFORMATION:
; APPLICANT: Boyle, William J.
; APPLICANT: Lacey, David L.
```



```
; APPLICANT: Calzone, Frank J.
; APPLICANT: Chang, Ming-Shi
; TITLE OF INVENTION: OSTEOPROTEGERIN
; NUMBER OF SEQUENCES: 53
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Amgen Inc.
; STREET: 1840 Dehavilland Drive
; CITY: Thousand Oaks
; STATE: California
; COUNTRY: USA
; ZIP: 91320-1789
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: PatentIn Release #1.0, Version #1.30
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/795,445A
; FILING DATE:
; CLASSIFICATION:
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: 08/577,788
; FILING DATE:
; ATTORNEY/AGENT INFORMATION:
; NAME: Winter, Robert B.
; REFERENCE/DOCKET NUMBER: A-378
; INFORMATION FOR SEQ ID NO: 48:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 227 amino acids
; TYPE: amino acid
; STRANDEDNESS: single
; TOPOLOGY: linear
; MOLECULE TYPE: protein
; US-08-795-445A-48

Query Match 26.9%; Score 305; DB 3; Length 227;
Best Local Similarity 35.0%; Pred. No. 3.9e-21;
Matches 70; Conservative 24; Mismatches 78; Indels 28; Gaps 9;

QY 5 AVPPYASE-NQTRDQEKYEYEPQHRICCSRCPPGYVSAAKSRIRDTVCATCAENSYN 63
Db |||||:||||:||||:||||:||||:||||:||||:||||:||||:||||:||||:
28 AFTPYAPEPGSTCR--LREYDQTAQMCCKSCSPGQHAQVFKTKTSDTVCDSCEDSTY 85
QY 64 HNNYLTICQLCR---PCDPVMGLEELIAPCTSKRKTQCRQCPGMFCAWALE-CTHCELLS 119
Db ||||:||||:||||:||||:||||:||||:||||:||||:||||:||||:||||:
86 LNNWVPECLSCGSRCSDDV---ETQACTREQNRICTCRPGMYCALSQKQEGCRLCAPLR 141
QY 120 DCPPG-----TEAELKDEVGKNNHCVPCKAGHFONTSSPSARCOPHTRCENQGLVEAAP 174
Db |||||:||||:||||:||||:||||:||||:||||:||||:||||:||||:||||:
142 KCRPGFGVARPGTETSDVV-----CKPCAPGTFSTNTSSDTCRPHQICN-----VVAIP 191
QY 175 GTAQSDTTC--KNPLEPLPP 192
Db |||||:||||:||||:||||:||||:||||:||||:||||:||||:||||:||||:
192 GNASRDVACTSTSPTRSMAP 211

RESULT 13
US-08-795-447A-48
; Sequence 48, Application US/08795447A
; Patent No. 6284728
; GENERAL INFORMATION:
; APPLICANT: Boyle, William J.
; APPLICANT: Lacey, David L.
; APPLICANT: Calzone, Frank J.
; APPLICANT: Chang, Ming-Shi
; TITLE OF INVENTION: Osteoprotegerin
; NUMBER OF SEQUENCES: 53
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Amgen Inc.
; STREET: One Amgen Center Drive
; CITY: Thousand Oaks
; STATE: California
; COUNTRY: USA

; APPLICANT: Calzone, Frank J.
; APPLICANT: Chang, Ming-Shi
; TITLE OF INVENTION: OSTEOPROTEGERIN
; NUMBER OF SEQUENCES: 53
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Amgen Inc.
; STREET: 1840 Dehavilland Drive
; CITY: Thousand Oaks
; STATE: California
; COUNTRY: USA
; ZIP: 91320-1789
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: PatentIn Release #1.0, Version #1.30
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/795,447A
; FILING DATE:
; CLASSIFICATION:
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: 08/577,788
; FILING DATE:
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; ZIP: 91362-1789
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: PatentIn Release #1.0, Version #1.30
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/795,447A
; FILING DATE:
; CLASSIFICATION: 514
; ATTORNEY/AGENT INFORMATION:
; NAME: Winter, Robert B.
; REFERENCE/DOCKET NUMBER: A-378D2
; INFORMATION FOR SEQ ID NO: 48:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 227 amino acids
; TYPE: amino acid
; STRANDEDNESS: single
; TOPOLOGY: linear
; MOLECULE TYPE: protein
; US-08-795-447A-48

Query Match 26.9%; Score 305; DB 3; Length 227;
Best Local Similarity 35.0%; Pred. No. 3.9e-21;
Matches 70; Conservative 24; Mismatches 78; Indels 28; Gaps 9;

QY 5 AVPPYASE-NQTRDQEKYEYEPQHRICCSRCPPGYVSAAKSRIRDTVCATCAENSYN 63
Db |||||:||||:||||:||||:||||:||||:||||:||||:||||:||||:||||:
28 AFTPYAPEPGSTCR--LREYDQTAQMCCKSCSPGQHAQVFKTKTSDTVCDSCEDSTY 85
QY 64 HNNYLTICQLCR---PCDPVMGLEELIAPCTSKRKTQCRQCPGMFCAWALE-CTHCELLS 119
Db ||||:||||:||||:||||:||||:||||:||||:||||:||||:||||:||||:
86 LNNWVPECLSCGSRCSDDV---ETQACTREQNRICTCRPGMYCALSQKQEGCRLCAPLR 141
QY 120 DCPPG-----TEAELKDEVGKNNHCVPCKAGHFONTSSPSARCOPHTRCENQGLVEAAP 174
Db |||||:||||:||||:||||:||||:||||:||||:||||:||||:||||:||||:
142 KCRPGFGVARPGTETSDVV-----CKPCAPGTFSTNTSSDTCRPHQICN-----VVAIP 191
QY 175 GTAQSDTTC--KNPLEPLPP 192
Db |||||:||||:||||:||||:||||:||||:||||:||||:||||:||||:||||:
192 GNASRDVACTSTSPTRSMAP 211

RESULT 14
US-08-974-186-48
; Sequence 48, Application US/08974186
; Patent No. 6284740
; GENERAL INFORMATION:
; APPLICANT: Boyle, William J.
; APPLICANT: Lacey, David L.
; APPLICANT: Calzone, Frank J.
; APPLICANT: Chang, Ming-Shi
; TITLE OF INVENTION: OSTEOPROTEGERIN
; NUMBER OF SEQUENCES: 53
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Amgen Inc.
; STREET: 1840 Dehavilland Drive
; CITY: Thousand Oaks
; STATE: California
; COUNTRY: USA
; ZIP: 91320-1789
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: PatentIn Release #1.0, Version #1.30
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/974,186
; FILING DATE:
; CLASSIFICATION:
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: 08/577,788
; FILING DATE:
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QY 61 YNEHWNLTICQLCRPCDPVWGKNNHCVPCKAGHFQNTSSPSARCPHTRCENQGLVEAAPGTAQSD 120
Db 61 YNEHWNLTICQLCRPCDPVWGKNNHCVPCKAGHFQNTSSPSARCPHTRCENQGLVEAAPGTAQSD 120
QY 121 CPFGTEAELKDEVGKNNHCVPCKAGHFQNTSSPSARCPHTRCENQGLVEAAPGTAQSD 180
Db 121 CPFGTEAELKDEVGKNNHCVPCKAGHFQNTSSPSARCPHTRCENQGLVEAAPGTAQSD 180
QY 181 TTCKNPLEPLPPMSGT 197
Db 181 TTCKNPLEPLPPMSGT 197

```

```

RESULT 2
US-10-077-406-1
; Sequence 1, Application US/10077406
; Publication No. US20050037003A1
; GENERAL INFORMATION:
; APPLICANT: Browning, et al.
; TITLE OF INVENTION: Soluble Lymphotoxin-B Receptors and Anti-lymphotoxin
; TITLE OF INVENTION: Receptor and Ligand Antibodies, as Therapeutic Agents
; TITLE OF INVENTION: for the Treatment of Immunological Disease.
; FILE REFERENCE: B191
; CURRENT APPLICATION NUMBER: US/10/077,406
; PRIOR FILING DATE: 2002-02-15
; PRIOR APPLICATION NUMBER: US/09/000,166
; PRIOR FILING DATE: 1998-06-08
; PRIOR APPLICATION NUMBER: PCT/US96/12010
; PRIOR FILING DATE: 1996-07-19
; NUMBER OF SEQ ID NOS: 3
; SOFTWARE: PatentIn Ver. 2.0
; SEQ ID NO 1
; LENGTH: 197
; TYPE: PRT
; ORGANISM: Homo sapiens
US-10-077-406-1

```

```

Query Match 100.0%; Score 1133; DB 17; Length 197;
Best Local Similarity 100.0%; Pred. No. 3.4e-86;
Matches 197; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 SQQAVPPYASENOTCRDQEKYEYEPQHRICCSRCPPGTYVSAAKCSRIKRTDTCATCAENS 60
Db 1 SQQAVPPYASENOTCRDQEKYEYEPQHRICCSRCPPGTYVSAAKCSRIKRTDTCATCAENS 60
QY 61 YNEHWNLTICQLCRPCDPVWGKNNHCVPCKAGHFQNTSSPSARCPHTRCENQGLVEAAPGTAQSD 120
Db 61 YNEHWNLTICQLCRPCDPVWGKNNHCVPCKAGHFQNTSSPSARCPHTRCENQGLVEAAPGTAQSD 120
QY 121 CPFGTEAELKDEVGKNNHCVPCKAGHFQNTSSPSARCPHTRCENQGLVEAAPGTAQSD 180
Db 121 CPFGTEAELKDEVGKNNHCVPCKAGHFQNTSSPSARCPHTRCENQGLVEAAPGTAQSD 180
QY 181 TTCKNPLEPLPPMSGT 197
Db 181 TTCKNPLEPLPPMSGT 197

```

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RESULT 3
US-09-907-372-19
; Sequence 19, Application US/09907372
; Patent No. US20020068242A1
; GENERAL INFORMATION:
; APPLICANT: Lal, Preeti G.
; APPLICANT: Warren, Bridget A.
; TITLE OF INVENTION: TNF RECEPTOR 2 RELATED PROTEIN VARIANT
; FILE REFERENCE: PC-0050 US
; CURRENT APPLICATION NUMBER: US/09/907,372
; CURRENT FILING DATE: 2001-07-27
; NUMBER OF SEQ ID NOS: 20
; SOFTWARE: PERL Program
; SEQ ID NO 19
; LENGTH: 435

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; TYPE: PRT
; ORGANISM: Homo sapiens
; FEATURE:
; NAME/KEY: misc feature
; OTHER INFORMATION: Incyte ID No. US20020068242A1 g339762
US-09-907-372-19

Query Match 100.0%; Score 1133; DB 9; Length 435;
Best Local Similarity 100.0%; Pred. No. 7.4e-86;
Matches 197; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 SQQAVPPYASENOTCRDQEKYEYEPQHRICCSRCPPGTYVSAAKCSRIKRTDTCATCAENS 60
Db 28 SQQAVPPYASENOTCRDQEKYEYEPQHRICCSRCPPGTYVSAAKCSRIKRTDTCATCAENS 87
QY 61 YNEHWNLTICQLCRPCDPVWGKNNHCVPCKAGHFQNTSSPSARCPHTRCENQGLVEAAPGTAQSD 120
Db 88 YNEHWNLTICQLCRPCDPVWGKNNHCVPCKAGHFQNTSSPSARCPHTRCENQGLVEAAPGTAQSD 147
QY 121 CPFGTEAELKDEVGKNNHCVPCKAGHFQNTSSPSARCPHTRCENQGLVEAAPGTAQSD 180
Db 148 CPFGTEAELKDEVGKNNHCVPCKAGHFQNTSSPSARCPHTRCENQGLVEAAPGTAQSD 207
QY 181 TTCKNPLEPLPPMSGT 197
Db 208 TTCKNPLEPLPPMSGT 224

```

```

RESULT 4
US-09-768-779A-6
; Sequence 6, Application US/09768779A
; Patent No. US20020127637A1
; GENERAL INFORMATION:
; APPLICANT: NI, JIAN
; APPLICANT: MOORE, PAUL
; TITLE OF INVENTION: HUMAN TUMOR NECROSIS FACTOR
; RECEPTOR-LIKE PROTEIN 8
; NUMBER OF SEQUENCES: 24
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: HUMAN GENOME SCIENCES, INC.
; STREET: 9410 KEY WEST AVENUE
; CITY: ROCKVILLE
; STATE: MD
; COUNTRY: US
; ZIP: 20850
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: PatentIn Release #1.0, Version #1.30
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/09/768,779A
; FILING DATE: 25-Jan-2001
; CLASSIFICATION: <Unknown>
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: 09/086,582
; FILING DATE: <Unknown>
; ATTORNEY/AGENT INFORMATION:
; NAME: KENLEY K. HOOVER
; REGISTRATION NUMBER: 40,302
; REFERENCE/DOCKET NUMBER: PF368PP
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: (301) 309-8504
; TELEFAX: (301) 309-8439
; INFORMATION FOR SEQ ID NO: 6:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 435 amino acids
; TYPE: amino acid
; STRANDEDNESS: single
; TOPOLOGY: linear
; MOLECULE TYPE: protein
; SEQUENCE DESCRIPTION: SEQ ID NO: 6:
US-09-768-779A-6

```

Query Match 100.0%; Score 1133; DB 9; Length 435;  
Best Local Similarity 100.0%; Pred. No. 7.4e-86;  
Matches 197; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 SQQAVPPYASENQTCDQKEYEYEPQHRICCSRCPPGTVVSAKCSRIKRTVTCATCAENS 60  
DB 28 SQQAVPPYASENQTCDQKEYEYEPQHRICCSRCPPGTVVSAKCSRIKRTVTCATCAENS 87

QY 61 YNEHWNLTICQLCRPCDPVMGLEEIAICTSKRTQCRQCPGMFCAAWALECTHCELLSD 120  
DB 88 YNEHWNLTICQLCRPCDPVMGLEEIAICTSKRTQCRQCPGMFCAAWALECTHCELLSD 147

QY 121 CPPTGEAEKDEVGKGNHCVCKAGHFQNTSSPSARCQPHTRCENQGLVEAAPGTAQSD 180  
DB 148 CPPTGEAEKDEVGKGNHCVCKAGHFQNTSSPSARCQPHTRCENQGLVEAAPGTAQSD 207

QY 181 TTCKNPLEPLPPMSGT 197  
DB 208 TTCKNPLEPLPPMSGT 224

## RESULT 5

US-09-917-372-19

; Sequence 19, Application US/09917372  
; Publication No. US20030068619A1  
; GENERAL INFORMATION:  
; APPLICANT: Lal, Preeti G.  
; APPLICANT: Warren, Bridget A.  
; TITLE OF INVENTION: TNF RECEPTOR 2 RELATED PROTEIN VARIANT  
; FILE REFERENCE: PC-0050 US  
; CURRENT APPLICATION NUMBER: US/09/917,372  
; NUMBER OF SEQ ID NOS: 20  
; SOFTWARE: PERL Program  
; SEQ ID NO 19  
; LENGTH: 435  
; TYPE: PRT  
; ORGANISM: Homo sapiens  
; NAME/KEY: misc feature  
; OTHER INFORMATION: Incyte ID No. US20030068619A1 g339762  
US-09-917-372-19

Query Match 100.0%; Score 1133; DB 10; Length 435;  
Best Local Similarity 100.0%; Pred. No. 7.4e-86;  
Matches 197; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 SQQAVPPYASENQTCDQKEYEYEPQHRICCSRCPPGTVVSAKCSRIKRTVTCATCAENS 60  
DB 28 SQQAVPPYASENQTCDQKEYEYEPQHRICCSRCPPGTVVSAKCSRIKRTVTCATCAENS 87

QY 61 YNEHWNLTICQLCRPCDPVMGLEEIAICTSKRTQCRQCPGMFCAAWALECTHCELLSD 120  
DB 88 YNEHWNLTICQLCRPCDPVMGLEEIAICTSKRTQCRQCPGMFCAAWALECTHCELLSD 147

QY 121 CPPTGEAEKDEVGKGNHCVCKAGHFQNTSSPSARCQPHTRCENQGLVEAAPGTAQSD 180  
DB 148 CPPTGEAEKDEVGKGNHCVCKAGHFQNTSSPSARCQPHTRCENQGLVEAAPGTAQSD 207

QY 181 TTCKNPLEPLPPMSGT 197  
DB 208 TTCKNPLEPLPPMSGT 224

## RESULT 6

US-10-087-192-942

; Sequence 942, Application US/10087192  
; Publication No. US20020182586A1  
; GENERAL INFORMATION:  
; APPLICANT: Morris, David W.  
; APPLICANT: Engelhard, Eric K.  
; TITLE OF INVENTION: NOVEL COMPOSITIONS AND METHODS FOR

; TITLE OF INVENTION: CANCER  
; FILE REFERENCE: 529452000122  
; CURRENT APPLICATION NUMBER: US/10/087,192  
; CURRENT FILING DATE: 2002-03-01  
; PRIOR APPLICATION NUMBER: US 09/747,377  
; PRIOR FILING DATE: 2000-12-22  
; PRIOR APPLICATION NUMBER: US 09/798,586  
; PRIOR FILING DATE: 2001-03-02  
; NUMBER OF SEQ ID NOS: 2059  
; SOFTWARE: FastSeq for Windows Version 4.0  
; SEQ ID NO 942  
; LENGTH: 435  
; TYPE: PRT  
; ORGANISM: Homo sapiens  
US-10-087-192-942

Query Match 100.0%; Score 1133; DB 13; Length 435;  
Best Local Similarity 100.0%; Pred. No. 7.4e-86;  
Matches 197; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 SQQAVPPYASENQTCDQKEYEYEPQHRICCSRCPPGTVVSAKCSRIKRTVTCATCAENS 60  
DB 28 SQQAVPPYASENQTCDQKEYEYEPQHRICCSRCPPGTVVSAKCSRIKRTVTCATCAENS 87

QY 61 YNEHWNLTICQLCRPCDPVMGLEEIAICTSKRTQCRQCPGMFCAAWALECTHCELLSD 120  
DB 88 YNEHWNLTICQLCRPCDPVMGLEEIAICTSKRTQCRQCPGMFCAAWALECTHCELLSD 147

QY 121 CPPTGEAEKDEVGKGNHCVCKAGHFQNTSSPSARCQPHTRCENQGLVEAAPGTAQSD 180  
DB 148 CPPTGEAEKDEVGKGNHCVCKAGHFQNTSSPSARCQPHTRCENQGLVEAAPGTAQSD 207

QY 181 TTCKNPLEPLPPMSGT 197  
DB 208 TTCKNPLEPLPPMSGT 224

## RESULT 7

US-10-291-480-6  
; Sequence 6, Application US/10291480  
; Publication No. US2003010069A1  
; GENERAL INFORMATION:  
; APPLICANT: Ni, Jian  
; APPLICANT: Moore, Paul  
; TITLE OF INVENTION: Human Tumor Necrosis Factor Receptor-Like Protein 8  
; FILE REFERENCE: PF368CJ1  
; CURRENT APPLICATION NUMBER: US/10/291,480  
; CURRENT FILING DATE: 2002-11-12  
; PRIOR APPLICATION NUMBER: 09/768,779  
; PRIOR FILING DATE: 2001-01-25  
; PRIOR APPLICATION NUMBER: 09/086,582  
; PRIOR FILING DATE: 1998-05-28  
; PRIOR APPLICATION NUMBER: 60/048,020  
; PRIOR FILING DATE: 1997-05-29  
; NUMBER OF SEQ ID NOS: 24  
; SOFTWARE: PatentIn version 3.1  
; SEQ ID NO 6  
; LENGTH: 435  
; TYPE: PRT  
; ORGANISM: human  
US-10-291-480-6

Query Match 100.0%; Score 1133; DB 14; Length 435;  
Best Local Similarity 100.0%; Pred. No. 7.4e-86;  
Matches 197; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 SQQAVPPYASENQTCDQKEYEYEPQHRICCSRCPPGTVVSAKCSRIKRTVTCATCAENS 60  
DB 28 SQQAVPPYASENQTCDQKEYEYEPQHRICCSRCPPGTVVSAKCSRIKRTVTCATCAENS 87

QY 61 YNEHWNLTICQLCRPCDPVMGLEEIAICTSKRTQCRQCPGMFCAAWALECTHCELLSD 120  
DB 88 YNEHWNLTICQLCRPCDPVMGLEEIAICTSKRTQCRQCPGMFCAAWALECTHCELLSD 147

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QY 121 CPPGTEAELKDEVGKGNHCVPCKAGHFQNTSSPSARCQPHTRCENQGLVEAAPGTAQSD 180
Db 148 CPPGTEAELKDEVGKGNHCVPCKAGHFQNTSSPSARCQPHTRCENQGLVEAAPGTAQSD 207
QY 181 TTCKNPLEPLPPMSGT 197
Db 208 TTCKNPLEPLPPMSGT 224

RESULT 8
US-10-369-300-17
; Sequence 17, Application US/10369300
; Publication No. US20030215442A1
; GENERAL INFORMATION:
; APPLICANT: Fraser, Christopher
; APPLICANT: Hancock, Wayne
; TITLE OF INVENTION: METHODS AND COMPOSITIONS FOR THE TREATMENT OR PREVENTION OF
; TITLE OF INVENTION: IMMUNE DISORDERS USING COMBINATION THERAPY
; FILE REFERENCE: 7853-255
; CURRENT APPLICATION NUMBER: US/10/369,300
; CURRENT FILING DATE: 2003-02-19
; PRIOR APPLICATION NUMBER: 60/358,463
; PRIOR FILING DATE: 2002-02-19
; NUMBER OF SEQ ID NOS: 23
; SOFTWARE: PatentIn version 3.1
; SEQ ID NO 17
; LENGTH: 435
; TYPE: PRT
; ORGANISM: Homo sapiens
US-10-369-300-17

Query Match 100.0%; Score 1133; DB 15; Length 435;
Best Local Similarity 100.0%; Pred. No. 7.4e-86;
Matches 197; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 SQQAVPPYASENQTCRDQEKYEYEPQHRICCSRCPGTYVSATKSRIRDTVCATCAENS 60
Db 28 SQQAVPPYASENQTCRDQEKYEYEPQHRICCSRCPGTYVSATKSRIRDTVCATCAENS 87
QY 61 YNEHWNLYTICQLCRPCDPVWGLEIAPCTSKRKTQCRQCPGMFCAAWALECTHCELLSD 120
Db 88 YNEHWNLYTICQLCRPCDPVWGLEIAPCTSKRKTQCRQCPGMFCAAWALECTHCELLSD 147
QY 121 CPPGTEAELKDEVGKGNHCVPCKAGHFQNTSSPSARCQPHTRCENQGLVEAAPGTAQSD 180
Db 148 CPPGTEAELKDEVGKGNHCVPCKAGHFQNTSSPSARCQPHTRCENQGLVEAAPGTAQSD 207
QY 181 TTCKNPLEPLPPMSGT 197
Db 208 TTCKNPLEPLPPMSGT 224

RESULT 9
US-10-262-445-133
; Sequence 133, Application US/10262445
; Publication No. US20040014058A1
; GENERAL INFORMATION:
; APPLICANT: Alsobrook II, John
; APPLICANT: Burgess, Catherine
; APPLICANT: Catterton, Elina
; APPLICANT: Chant, John
; APPLICANT: Chaudhuri, Amitabha
; APPLICANT: Edinger, Shlomit
; APPLICANT: Gerlach, Valerie
; APPLICANT: Giot, Loic
; APPLICANT: Gorman, Linda
; APPLICANT: Guo, Xiaojia
; APPLICANT: Kekuda, Ramesh
; APPLICANT: Mezes, Peter
; APPLICANT: Millet, Isabelle
; APPLICANT: Ooi, Chean Eng
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; APPLICANT: Patturajan, Meera
; APPLICANT: Rieger, Daniel
; APPLICANT: Spytek, Kimberly
; APPLICANT: Taupier Jr., Raymond J.
; APPLICANT: Zerhusen, Bryan
; APPLICANT: Zhong, Haihong
; APPLICANT: Zhong, Mei
; TITLE OF INVENTION: NOVEL HUMAN PROTEINS, POLYNUCLEOTIDES ENCODING THEM AND METHODS
; FILE REFERENCE: 21402-462D
; CURRENT APPLICATION NUMBER: US/10/262,445
; CURRENT FILING DATE: 2002-10-01
; PRIOR APPLICATION NUMBER: 60/327,454
; PRIOR FILING DATE: 2001-10-05
; PRIOR APPLICATION NUMBER: 60/327,917
; PRIOR FILING DATE: 2001-10-09
; PRIOR APPLICATION NUMBER: 60/328,029
; PRIOR FILING DATE: 2001-10-09
; PRIOR APPLICATION NUMBER: 60/328,056
; PRIOR FILING DATE: 2001-10-09
; PRIOR APPLICATION NUMBER: 60/328,849
; PRIOR FILING DATE: 2001-10-12
; PRIOR APPLICATION NUMBER: 60/329,414
; PRIOR FILING DATE: 2001-10-15
; PRIOR APPLICATION NUMBER: 60/330,142
; PRIOR FILING DATE: 2001-10-17
; PRIOR APPLICATION NUMBER: 60/341,058
; PRIOR FILING DATE: 2001-10-22
; PRIOR APPLICATION NUMBER: 60/343,629
; PRIOR FILING DATE: 2001-10-24
; PRIOR APPLICATION NUMBER: 60/349,575
; PRIOR FILING DATE: 2001-10-29
; Remaining Prior Application data removed - See File Wrapper or PALM.
; NUMBER OF SEQ ID NOS: 133
; SOFTWARE: CuraSeqList version 0.1
; SEQ ID NO 133
; LENGTH: 435
; TYPE: PRT
; ORGANISM: Homo sapiens
US-10-262-445-133

Query Match 100.0%; Score 1133; DB 15; Length 435;
Best Local Similarity 100.0%; Pred. No. 7.4e-86;
Matches 197; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 SQQAVPPYASENQTCRDQEKYEYEPQHRICCSRCPGTYVSATKSRIRDTVCATCAENS 60
Db 28 SQQAVPPYASENQTCRDQEKYEYEPQHRICCSRCPGTYVSATKSRIRDTVCATCAENS 87
QY 61 YNEHWNLYTICQLCRPCDPVWGLEIAPCTSKRKTQCRQCPGMFCAAWALECTHCELLSD 120
Db 88 YNEHWNLYTICQLCRPCDPVWGLEIAPCTSKRKTQCRQCPGMFCAAWALECTHCELLSD 147
QY 121 CPPGTEAELKDEVGKGNHCVPCKAGHFQNTSSPSARCQPHTRCENQGLVEAAPGTAQSD 180
Db 148 CPPGTEAELKDEVGKGNHCVPCKAGHFQNTSSPSARCQPHTRCENQGLVEAAPGTAQSD 207
QY 181 TTCKNPLEPLPPMSGT 197
Db 208 TTCKNPLEPLPPMSGT 224

RESULT 10
US-09-907-372-1
; Sequence 1, Application US/09907372
; Patent No. US20020068242A1
; GENERAL INFORMATION:
; APPLICANT: Ial, Preeti G.
; APPLICANT: Warren, Bridget A.
; TITLE OF INVENTION: TNF RECEPTOR 2 RELATED PROTEIN VARIANT
; FILE REFERENCE: PC-0050 US
; CURRENT APPLICATION NUMBER: US/09/907,372
; CURRENT FILING DATE: 2001-07-27
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; NUMBER OF SEQ ID NOS: 20
; SOFTWARE: PERL Program
; SEQ ID NO 1
; LENGTH: 399
; TYPE: PRT
; ORGANISM: Homo sapiens
; FEATURE:
; NAME/KEY: misc feature
; OTHER_INFORMATION: Incy
US-09-907-372-1

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Query Match          99.6%; Score 1129; DB 9; Length 399;
Best Local Similarity 99.5%; Pred. NO. 1.5e-85;
Matches 196; Conservative 1; Mismatches 0; Indels 0; Gaps 0;
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RESULT 11  
US-09-917-372-1  
; Sequence 1, Application US/09917372

Query Match 99.6%; Score 1129; DB 10; Length 399;  
Best Local Similarity 99.5%; Pred. No. 1.5e-85;  
Matches 196; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

RESULT 12  
US-10-484-148-16  
; Sequence 16, Application US/10484148  
; Publication No. US20040248251A1  
; GENERAL INFORMATION:  
; APPLICANT: LAL, Preeti G.; HONCHELL, Cynthia D.;  
; APPLICANT: FORSYTHE, Ian J.; CHAMLA, Narinder K.;  
; APPLICANT: TANG, Y. Tom; BOROWSKY, Mark L.; BARROSO, Ines;  
; APPLICANT: YUE, Henry; WARREN, Bridget A.;  
; APPLICANT: THANGAVEJULU, Kavitha; GIETZEN, Kimberly J.;  
; APPLICANT: AZIMZAI, Yalida; LEE, Ernestine A.;  
; APPLICANT: BAUGHN, Mariah R.; GORVAD, Ann E.;  
; APPLICANT: DUGGAN, Brendan M.; TRAN, Bao;  
; APPLICANT: LI, Joana X.; RICHARDSON, Thomas W.;  
; APPLICANT: ELLIOTT, Vicki S.; ZEBARZADIAN, Yeganeh  
; APPLICANT: TRAN, Uyen K.; YAO, Monique G.;  
; APPLICANT: PETERSON, David P.; LUO, Wen  
; APPLICANT: LEHR-MASON, Patricia M.  
; TITLE OF INVENTION: RECEPTORS AND MEMBRANE ASSOCIATED PROTEINS  
; FILE REFERENCE: PF-1082 USN  
; CURRENT APPLICATION NUMBER: US/10/484. 148

Query Match	97.8%	Score 1108;	DB 16;	Length 416;			
Best Local Similarity	100.0%;	Prod. No. 8.4e-84;					
Matches 192;	Conservative 0;	Mismatches 0;	Indels 0;	Gaps 0;			
Qy	6	VPVYASENQTRQOEKEYEYEPQHRICCSRCPGPGTYVSAAKCSRI	RD	TVCATCAENSYN	65		
Db	14	VPVYASENQTRQOEKEYEYEPQHRICCSRCPGPGTYVSAAKCSRI	RD	TVCATCAENSYN	73		
Qy	66	NYLTIQOLCRPCDPVWMLGBIA	PC	TSKRTQCRQPGMFCNAWALECTHCELLSDCP	125		
Db	74	NYLTIQOLCRPCDPVWMLGBIA	PC	TSKRTQCRQPGMFCNAWALECTHCELLSDCP	133		
Qy	126	EAELEKDEVGKGNHCV	PC	KAGHFONTSSPSAR	CO	PHTRCENQGLVEAAPGTAQSDTTCKN	185
Db	134	EAELEKDEVGKGNHCV	PC	KAGHFONTSSPSAR	CO	PHTRCENQGLVEAAPGTAQSDTTCKN	193
Qy	186	PLEPLPLPPMSGT	197				

Db 194 PLEPLPPMSGT 205

## RESULT 13

US-10-112-793-14  
; Sequence 14, Application US/10112793  
; Publication No. US20020192729A1  
; GENERAL INFORMATION:

; APPLICANT: Ashkenazi, Avi J.  
; TITLE OF INVENTION: Apo-2 LI AND Apo-3 POLYPEPTIDES  
; NUMBER OF SEQUENCES: 28  
; CORRESPONDENCE ADDRESS:  
; ADDRESSEE: Genentech, Inc.  
; STREET: 1 DNA Way  
; CITY: South San Francisco  
; STATE: California  
; COUNTRY: USA  
; ZIP: 94080

## COMPUTER READABLE FORM:

; MEDIUM TYPE: 3.5 inch, 1.44 Mb floppy disk  
; COMPUTER: IBM PC compatible  
; OPERATING SYSTEM: PC-DOS/MS-DOS  
; SOFTWARE: WinPatin (Genentech)  
; CURRENT APPLICATION DATA:

; APPLICATION NUMBER: US/10/112,793

; FILING DATE: 28-Mar-2002

; CLASSIFICATION: <Unknown>

## PRIOR APPLICATION DATA:

; APPLICATION NUMBER: US/08/828,683A

; FILING DATE: 31-Mar-1997

; APPLICATION NUMBER: 08/625328

; FILING DATE: 1-Apr-1996

; APPLICATION NUMBER: 08/710802

; FILING DATE: 23-Sep-1996

## ATTORNEY/AGENT INFORMATION:

; NAME: Marschang, Diane L.

; REGISTRATION NUMBER: 35,600

; REFERENCE/DOCKET NUMBER: P1007P1

## TELECOMMUNICATION INFORMATION:

; TELEPHONE: 650/225-5416

; TELEFAX: 650/952-9881

; INFORMATION FOR SEQ ID NO: 14:

; SEQUENCE CHARACTERISTICS:

; LENGTH: 170 amino acids

; TYPE: Amino Acid

; TOPOLOGY: Linear

; SEQUENCE DESCRIPTION: SEQ ID NO: 14:

US-10-112-793-14

Query Match 87.1%; Score 987; DB 13; Length 170;  
Best Local Similarity 100.0%; Pred. No. 3.8e-74; Indels 0; Gaps 0;  
Matches 170; Conservative 0; Mismatches 0;

QY 15 TCRDQKEYEYPOHRICCSRCPGTYVSACSRIRDTVCATCAENSYNEHWNLYTICQLC 74

Db 1 TCRDQKEYEYPOHRICCSRCPGTYVSACSRIRDTVCATCAENSYNEHWNLYTICQLC 60

QY 75 RCPDPVWGLEEIIAPCTSKRTQCRCPGMFCAAWALECTHCELLSDCPPGTEAEIKDEVG 134

Db 61 RCPDPVWGLEEIIAPCTSKRTQCRCPGMFCAAWALECTHCELLSDCPPGTEAEIKDEVG 120

QY 135 KGNHNCVPCKAGHFONTSSPSARCQPHTRCENQGLVEAAPGTAQSDTTCK 184

Db 121 KGNHNCVPCKAGHFONTSSPSARCQPHTRCENQGLVEAAPGTAQSDTTCK 170

## RESULT 14

US-10-375-680-57

; Sequence 57, Application US/10375680

; Publication No. US20040009147A1

; GENERAL INFORMATION:

; APPLICANT: Ebner, Reinhard

; APPLICANT: Yu, Guo-Liang

; APPLICANT: Ruben, Steven M  
; APPLICANT: Ullrich, Stephen  
; APPLICANT: Zhai, Yifan  
; TITLE OF INVENTION: Apoptosis Inducing Molecule II and Methods of Use  
; FILE REFERENCE: 1488.065000E  
; CURRENT APPLICATION NUMBER: US/10/375,680  
; CURRENT FILING DATE: 2003-02-28  
; PRIOR APPLICATION NUMBER: US 60/360,234  
; PRIOR FILING DATE: 2002-03-01  
; NUMBER OF SEQ ID NOS: 70  
; SOFTWARE: PatentIn version 3.2  
; SEQ ID NO 57  
; LENGTH: 172  
; TYPE: PRT  
; ORGANISM: Homo sapiens  
; FEATURE:  
; NAME/KEY: misc feature  
; LOCATION: (7)-(7)  
; OTHER INFORMATION: Xaa can be any naturally occurring amino acid  
; US-10-375-680-57

Query Match 85.6%; Score 970; DB 15; Length 172;  
Best Local Similarity 98.3%; Pred. No. 1e-72; Indels 2; Gaps 1;  
Matches 169; Conservative 0; Mismatches 1;

QY 15 TCRDQEE--KEYEYPOHRICCSRCPGTYVSACSRIRDTVCATCAENSYNEHWNLYTICQ 72

Db 1 TCRDQEXAAEYEPQHRICCSRCPGTYVSACSRIRDTVCATCAENSYNEHWNLYTICQ 60

QY 73 LCRPCDPVWGLEEIIAPCTSKRTQCRCPGMFCAAWALECTHCELLSDCPPGTEAEIKDE 132

Db 61 LCRPCDPVWGLEEIIAPCTSKRTQCRCPGMFCAAWALECTHCELLSDCPPGTEAEIKDE 120

QY 133 VGKGNHNCVPCKAGHFONTSSPSARCQPHTRCENQGLVEAAPGTAQSDTTCK 184

Db 121 VGKGNHNCVPCKAGHFONTSSPSARCQPHTRCENQGLVEAAPGTAQSDTTCK 172

## RESULT 15

US-09-948-018-19

; Sequence 19, Application US/09948018

; Patent No. US20020150977A1

; GENERAL INFORMATION:

; APPLICANT: Theill et al

; TITLE OF INVENTION: TNF RECEPTOR-LIKE MOLECULES AND USES THEREOF

; FILE REFERENCE: 01017/37677

; CURRENT APPLICATION NUMBER: US/09/948,018

; CURRENT FILING DATE: 2001-09-05

; PRIOR APPLICATION NUMBER: US 60/230,191

; PRIOR FILING DATE: 2000-09-05

; NUMBER OF SEQ ID NOS: 45

; SOFTWARE: PatentIn version 3.1

; SEQ ID NO 19

; LENGTH: 257

; TYPE: PRT

; ORGANISM: Mus musculus

US-09-948-018-19

Query Match 68.8%; Score 780; DB 9; Length 257;

Best Local Similarity 100.0%; Pred. No. 8.7e-57;

Matches 135; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 63 EHWNYLTICQLCRPCDPVWGLEEIIAPCTSKRTQCRCPGMFCAAWALECTHCELLSDCP 122

Db 1 EHWNYLTICQLCRPCDPVWGLEEIIAPCTSKRTQCRCPGMFCAAWALECTHCELLSDCP 60

QY 123 PGTEAEIKDEYKGNHNCVPCKAGHFONTSSPSARCQPHTRCENQGLVEAAPGTAQSDTT 182

Db 61 PGTEAEIKDEYKGNHNCVPCKAGHFONTSSPSARCQPHTRCENQGLVEAAPGTAQSDTT 120

QY 183 CKNPLEPLPPMSGT 197

Db 121 CKNPLEPLPPMSGT 135

Search completed: September 23, 2005, 10:33:18  
Job time : 66 secs

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OM protein - protein search, using sw model

Run on: September 23, 2005, 09:46:31 ; Search time 40 Seconds  
(without alignments)  
473.868 Million cell updates/sec

Title: US-10-077-406-1

Perfect score: 1133

Sequence: 1 SQPQAVPPYASENQTCDQEE.....QSDTTCKNPLEPLPPMSGT 197

Scoring table: BLOSUM62

Gapop 10.0 , Gapext 0.5

Searched: 283416 seqs, 96216763 residues

Total number of hits satisfying chosen parameters: 283416

Minimum DB seq length: 0

Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%

Maximum Match 100%

Listing first 45 summaries

Database :

PIR 79:\*

1: pir1:\*

2: pir2:\*

3: pir3:\*

4: pir4:\*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	ID	Description
1	1133	100.0	435	1 I54182	tumor necrosis fac
2	305	26.9	461	1 A35356	tumor necrosis fac
3	295	26.0	474	2 B38634	tumor necrosis fac
4	290	25.6	459	2 I48854	gene murine tumour
5	278	24.5	277	2 A60771	B-cell activation
6	243.5	21.5	305	2 A46476	B cell-associated
7	226.5	20.0	651	2 JC7705	death receptor-6 -
8	222.5	19.6	271	2 S12783	OX40 antigen precu
9	214.5	18.9	272	2 I48700	gene ox40 protein
10	210.5	18.6	455	1 GQUT1	tumor necrosis fac
11	210	18.5	348	2 T28623	hypothetical prote
12	210	18.5	349	2 D36858	gene G4R protein -
13	207	18.3	349	2 D72175	G2R protein - vari
14	206	18.2	461	2 JC4302	tumor necrosis fac
15	201	17.7	277	2 I37552	OX40 homolog - hum
16	201	17.7	454	1 GQMT1	tumor necrosis fac
17	196	17.3	595	2 A42086	CD30 antigen precu
18	195.5	17.3	255	2 I38426	lymphocyte activat
19	189	16.7	325	2 B43692	T2 protein - rabbi
20	187.5	16.5	314	2 I37383	FAS soluble protei
21	184.5	16.3	461	1 GQUT1	tumor necrosis fac
22	183.5	16.2	326	1 GQVZML	T2 protein - myxom
23	181	16.0	335	2 A40036	apoptosis-mediati
24	179.5	15.8	256	2 B32393	T-cell antigen 4-1
25	171.5	15.1	425	1 A26431	nerve growth facto
26	166	14.7	493	2 JC5486	membrane glycoprot
27	164	14.5	416	1 JN0006	nerve growth facto
28	162	14.3	327	2 A46484	apoptosis-mediati
29	148.5	13.1	427	1 GQHUN	nerve growth facto

30	145.5	12.8	324	2 JC2395	Fas antigen precu
31	133	11.7	260	1 A46517	CD27 antigen precu
32	132.5	11.7	2	T26972	hypothetical prote
33	129.5	11.4	1620	2 T27283	hypothetical prote
34	129	11.4	3084	1 MMMSA	laminin alpha-1 ch
35	128.5	11.3	1299	2 T43251	furin (EC 3.4.21.7
36	128	11.3	1274	2 T42017	cysteine rich prot
37	126	11.1	3635	2 T10053	laminin alpha 5 ch
38	125.5	11.1	2180	2 T29764	hypothetical prote
39	124.5	11.0	899	2 G02428	subtilisin-like pr
40	124.5	11.0	915	2 JC6148	subtilisin-like pr
41	124.5	11.0	3707	2 S18252	heparan sulfate pr
42	124	10.9	1680	2 A43434	furin (EC 3.4.21.7
43	123.5	10.9	686	2 JC7569	DELTA-4 protein -
44	123	10.9	722	2 I48324	DELTA-like 1 - mou
45	122.5	10.8	915	1 A48225	subtilisin-like pr

ALIGNMENTS

RESULT 1

I54182

tumor necrosis factor receptor 2-related protein - human

C:Species: Homo sapiens (man)

C>Date: 24-May-1996 #sequence\_revision 24-May-1996 #text\_change 09-Jul-2004

C/Accession: I54182

R/Baens, M.; Chaffanet, M.; Cassiman, J.J.; Van den Berghe, H.; Marynen, P.

Genomics 16, 214-218, 1993.

A>Title:--Construction-and-evaluation of a hncDNA library of human l2p transcribed sequ

A/Reference number: I54182; MUID:93252381; PMID:8486360

A/Accession: I54182

A>Status: preliminary; translated from GB/EMBL/DDBJ

A/Molecule type: mRNA

A/Residues: 1-435 <RES>

A/Cross-references: UNIPROT:P36941; GB:I04270; NID:G339761; PIDN:AAA36757.1; PID:G33976

C/Genetics:

A/Gene: GDB:LTBR

A/Cross-references: GDB:1230195; OMIM:600979

A/Map position: l2p13.3-12p13.1

C/Superfamily: tumor necrosis factor receptor type 1 (TNFR1); NGF receptor repeat homol

Query Match	100.0%	Score 1133;	DB 2;	Length 435;
Best Local Similarity	100.0%;	Pred. No. 5.8e-78;		
Matches 197;	Conservative 0;	Mismatches 0;	Indels 0;	Gaps 0;
QY	1	SQPQAVPPYASENQTCDQEEKEYEYEPQHRICCSRCPPGTYVSAKCSRIIRDVTVCATCAENS	60	
DB	28	SQPQAVPPYASENQTCDQEEKEYEYEPQHRICCSRCPPGTYVSAKCSRIIRDVTVCATCAENS	87	
QY	61	YNEHWNYLTICQLCRPCDPVMGLEETAPCTSKRKTQCRQCPGMFCAWALECTHCLLSLD	120	
DB	88	YNEHWNYLTICQLCRPCDPVMGLEETAPCTSKRKTQCRQCPGMFCAWALECTHCLLSLD	147	
QY	121	CPFGTEAEALKDEVGKNNHCVPCKAGHFQNTSPSARCQPHTRCENQGLVEAAGTQASD	180	
DB	148	CPFGTEAEALKDEVGKNNHCVPCKAGHFQNTSPSARCQPHTRCENQGLVEAAGTQASD	207	
QY	181	TTCKNPLEPLPPMSGT 197		
DB	208	TTCKNPLEPLPPMSGT 224		

RESULT 2

A35356

tumor necrosis factor receptor 2 precursor [validated] - human

N/Alternate names: 75K tumor necrosis factor receptor; TNF receptor type 2

C:Species: Homo sapiens (man)

C>Date: 10-Sep-1999 #sequence\_revision 10-Sep-1999 #text\_change 09-Jul-2004

C/Accession: A35356; A36475; A48416; A36007; A23666; B35010; I38094

R/Smith, C.A.; Davis, T.; Anderson, D.; Solam, L.; Beckmann, M.P.; Jerzy, R.; Dower, S.

Science 248, 1019-1023, 1990

A>Title: A receptor for tumor necrosis factor defines an unusual family of cellular and



Db 90 QFTCLSCSSCTDQV---ETRACTKQONRVCAACEAGRYCALKTHSGSCRCQWLSKC 145  
 QY 122 PGTEAELKDEVGKGNHCVCKAGHFONTSSPSPARCOPHTRCENOGLVAAAPGTAQSDT 181  
 Db 146 GGF-GVASSRPNAGNVLCACAPGTFTSDTSDVCRPHRCS-----ILAIPGNASTDA 200  
 QY 182 TCKNPLEPLPPMS 195  
 Db 201 VC-----APESPTLS 210

RESULT 4  
 I48854  
 gene murine tumour necrosis factor receptor 2 protein - mouse (fragment)  
 C:Species: Mus musculus (house mouse)  
 C>Date: 02-Jul-1996 #sequence\_revision 02-Jul-1996 #text\_change 09-Jul-2004  
 C:Accession: I48854  
 R:Powell, E.B.; Wicker, L.S.; Peterson, L.B.; Todd, J.A.  
 Mamm. Genome 5, 726-727, 1994  
 A:Title: Allelic variation of the type 2 tumor necrosis factor receptor gene.  
 A:Reference number: I48854; MUID:95178848; PMID:7873884  
 A:Accession: I48854  
 A>Status: preliminary; translated from GB/EMBL/DBJ  
 A:Molecule type: mRNA  
 A:Residues: 1-459 <RES>  
 A:Cross-references: UNIPROT:Q62327; EMBL:X76401; NID:9433830; PIDN:CAA53981.1; PID:94338  
 C:Superfamily: tumor necrosis factor receptor type 2 (TNFR2); NGF receptor repeat homology  
 P:151-188/Domain: NGF receptor repeat homology <NGF>

Query Match 25.6%; Score 290; DB 2; Length 459;  
 Best Local Similarity 33.5%; Pred. No. 1e-14;  
 Matches 65; Conservative 24; Mismatches 85; Indels 20; Gaps 8;

QY 8 PYASE-NQTCRQDEKEYEYEPQHRICCSRCPPTGYTVSAKSRIRDTVCATCAENSNEHWN 66  
 Db 16 PYKPEPGYEQISQ-EYDRKQMCCKACPGQGVYKHFNCNKTSDTVCADCEASMTQVWN 74  
 QY 67 YLTICQLCR---PCDPVMGLEBIEAPCTSKRKTQCRQCPGMFCA--AWALECTHCELLSDC 121  
 Db 75 QFTCLSCSSCTDQV---ETRACTKQONRVCAACEAGRYCALKTHSGSCRCQWLSKC 130  
 QY 122 PGTEAELKDEVGKGNHCVCKAGHFONTSSPSPARCOPHTRCENOGLVAAAPGTAQSDT 181  
 Db 131 GGF-GVASSRPNAGNVLCACAPGTFTSDTSDVCRPHRCS-----ILAIPGNASTDA 185  
 QY 182 TCKNPLEPLPPMS 195  
 Db 186 VC-----APESPTLS 195

RESULT 5  
 A60771  
 B-cell activation protein CD40 precursor - human  
 N:Alternate names: B-cell surface antigen Bp50  
 C:Species: Homo sapiens (man)  
 C>Date: 03-Jun-1993 #sequence\_revision 03-Feb-1994 #text\_change 09-Jul-2004  
 C:Accession: S04460; A60771  
 R:Stamenkovic, I.; Clark, E.A.; Seed, B.  
 EMBO J. 8, 1403-1410, 1989  
 A:Title: A B-lymphocyte activation molecule related to the nerve growth factor receptor  
 A:Reference number: S04460; MUID:89356608; PMID:2475341  
 A:Accession: S04460  
 A:Molecule type: mRNA  
 A:Residues: 1-277 <STA>  
 A:Cross-references: UNIPROT:P25942; EMBL:X60592; NID:929850; PIDN:CAA43045.1; PID:929851  
 R:Brasch-Andersen, S.; Paulie, S.; Koho, H.; Nika, H.; Aspenstroem, P.; Perlmann, P.  
 J. Immunol. 142, 562-567, 1989  
 A:Title: Biochemical characteristics and partial amino acid sequence of the receptor-like  
 A:Reference number: A60771; MUID:89093941; PMID:2463309  
 A:Accession: A60771  
 A:Molecule type: protein  
 A:Residues: 21-50 <BRA>

A:Experimental source: Burkitt lymphoma cell line Raji  
 C:Genetic:  
 A:Gene: GDB:CD40  
 A:Cross-references: GDB:215268; OMIM:109535  
 A:Map position: 20q12-20q13.2  
 C:Superfamily: CD27 antigen; NGF receptor repeat homology  
 C:Keywords: B-cell; glycoprotein; phosphoprotein; surface antigen; transmembrane protein.  
 F:1-20/Domain: signal sequence #status predicted <SIG>  
 F:21-193/Domain: B-cell activation protein CD40 #status experimental <MAT>  
 F:21-193/Domain: extracellular #status predicted <EXT>  
 F:194-215/Domain: transmembrane #status predicted <TM>  
 F:216-277/Domain: intracellular #status predicted <CYT>  
 F:153,180/Binding site: carbohydrate (Aen) (covalent) #status predicted

Query Match 24.5%; Score 278; DB 2; Length 277;  
 Best Local Similarity 35.0%; Pred. No. 5.5e-14;  
 Matches 62; Conservative 20; Mismatches 83; Indels 12; Gaps 5;

QY 7 PPVASENQTCRQDEKEYEYEPQHRICCSRCPPTGYTVSAKSRIRDTVCATCAENSNEHWN 66  
 Db 22 PPTA-----CR--EQYLINSQ--CCSLCQPGQKLVSDCTETETETCLPGSESEFLDTWN 72  
 QY 67 YLTICQLCRPCDPVMGLEBIEAPCTSKRKTQCRQCPGMFCAAWALECTHCELLSDCPCPGTE 126  
 Db 73 RETHCHQHKYCDPNLGLRVQKGTSETDTICTCEGWHCTSEA--CESCVLHRSCTSPGFG 130  
 QY 127 AELKDEVGKGNHCVCKAGHFONTSSPSPARCOPHTRCENOGLVAAAPGTAQSDTTC 183  
 Db 131 VK-QIATGVSDTICPCPVGPFPSNVSSAFKCHPMTSCETKOLVQQAGTKNTKDVVC 186

RESULT 6  
 A46476  
 B cell-associated surface molecule CD40, long splice form - mouse  
 C:Species: Mus musculus (house mouse)  
 C>Date: 18-Jun-1993 #sequence\_revision 18-Nov-1994 #text\_change 09-Jul-2004  
 C:Accession: A46476; A46515  
 R:Torres, R.M.; Clark, E.A.  
 J. Immunol. 148, 620-626, 1992  
 A:Title: Differential increase of an alternatively polyadenylated mRNA species of murin.  
 A:Reference number: A46476; MUID:92105763; PMID:1370315  
 A:Accession: A46476  
 A:Molecule type: mRNA  
 A>Status: preliminary  
 A:Residues: 1-305 <TOR>  
 A:Cross-references: UNIPROT:P27512; GB:M83312; NID:91553058  
 A:Note: sequence extracted from NCBI backbone (NCBIN:75206, NCBI:P:75207)  
 A:Note: this translation is not annotated in GenBank entry MUSCD40A, release 113.0  
 R:Grimaldi, J.C.; Torres, R.; Kozak, C.A.; Chang, R.; Clark, E.A.; Howard, M.; Cockayne, J.  
 J. Immunol. 149, 3921-3926, 1992  
 A:Title: Genomic structure and chromosomal mapping of the murine CD40 gene.  
 A:Reference number: A46515; MUID:93094586; PMID:1281194  
 A:Accession: A46515  
 A>Status: preliminary; not compared with conceptual translation  
 A:Molecule type: nucleic acid  
 A:Residues: 1-287, 'LV', <GRI>  
 A:Cross-references: GB:M83312; NID:91553058; PIDN:AAB08705.1; PID:91553059; GB:M94126; I48854  
 A:Experimental source: BALB/c, liver  
 A:Note: sequence extracted from NCBI backbone (NCBI:P:120357)  
 C:Comment: For an alternative splice form, see PIR:A46515.  
 C:Comment: For an alternative splice form, see PIR:A46476.  
 C:Superfamily: CD27 antigen; NGF receptor repeat homology  
 C:Keywords: alternative splicing; transmembrane protein  
 F:105-144/Domain: NGF receptor repeat homology <NGF>

Query Match 21.5%; Score 243.5; DB 2; Length 305;  
 Best Local Similarity 31.0%; Pred. No. 2.3e-11;  
 Matches 54; Conservative 22; Mismatches 81; Indels 17; Gaps 5;

QY 15 TCRDQKEYEYEPQHRICCSRCPPTGYTVSAKSRIRDTVCATCAENSNEHWNVLTICQLC 74  
 Db 25 TCSD--KQYLHDGQ--CCDLCQPGSRLTSHCTALEKTOCHPCDSGFSQAQWNRIRCHQH 80







hypothetical protein G2R - variola major virus  
C:Species: variola major virus  
C:Date: 22-Oct-1999 #sequence\_revision 22-Oct-1999 #text\_change 09-Jul-2004  
C:Accession: T28623  
R:Massung, R.F.; Esposito, J.J.; Liu, L.I.; Qi, J.; Utterback, T.R.; Knight, J.C.; Aubin Nature 366, 748-751, 1993  
A:Title: Potential virulence determinants in terminal regions of variola smallpox virus  
A:Reference number: Z20488; MUID:94088747; PMID:8264798  
A:Accession: T28623  
A:Status: preliminary; translated from GB/EMBL/DBJ  
A:Molecule type: DNA  
A:Residues: 1-348 <NAS>  
A:Cross-references: UNIPROT:P34015; EMBL:L22579; NID:g623595; PIDN:AAA60933.1; PID:g4391  
A:Experimental source: strain Bangladesh 1975  
C:Superfamily: TNF-alpha receptor-II, vaccinia C22L type; NGF receptor repeat homology

Query Match 18.5%; Score 210; DB 2; Length 348;  
Best Local Similarity 29.0%; Pred. No. 8.3e-09;  
Matches 45; Conservative 20; Mismatches 80; Indels 10; Gaps 5;

QY 8 PYASENQTRDOEKYEYEPQHRICCSRCPPGTYVS AKSRIRDVTCATCAENSYNHNY 67  
DB 23 PYTPNGKCKDTEYK----RHNLCCLSCPPGTYASRLCDSKTNTQCTPCGSGTFTSRNNH 78  
QY 68 LTICQLCR-PCDPVMGLEIAPCTSKRKTQCRCPGMFC-AAWALECTHCELLSDCPPGT 125  
DB 79 LPACLSNCRGN--SNQVETRSCNTHNRICEPSGYCLLKGGSGCKACVSQTKC--GI 134  
QY 126 EAELEKDEVGKNNHCVPCKAGHFQNTSSPSARCP 160  
DB 135 GYGVSHTSVGDVICSPCGFGTYSHTVSSADKCEP 169

RESULT 12  
D36858  
Gene G4R protein - variola virus  
N:Alternate names: B28R protein (COP)  
C:Species: variola virus  
C:Date: 30-Sep-1993 #sequence\_revision 30-Sep-1993 #text\_change 09-Jul-2004  
C:Accession: D36858; S46888; S32385; S35987  
R:Blinov, V.M.  
submitted to GenBank, November 1992  
A:Reference number: A36859  
A:Accession: D36858  
A:Status: preliminary  
A:Molecule type: DNA  
A:Residues: 1-349 <BLI>  
A:Cross-references: UNIPROT:P34015; GB:X69198; NID:g456758; PIDN:CAA49137.1; PID:g457087  
A:Experimental source: strain India-1967, ssp. major, isolate Ind3  
R:Kolykhalov, A.A.; Blinov, V.M.; Gytarov, V.V.; Pozdnyakov, S.G.; Chizhikov, V.E.; Frolov submitted to the EMBL Data Library, April 1992  
A:Description: Nucleotide sequence analysis of the region of Variola virus XhoI F O H P  
A:Reference number: S46868  
A:Accession: S46888  
A:Status: preliminary  
A:Molecule type: DNA  
A:Residues: 1-349 <KOL>  
A:Cross-references: EMBL:X67117; NID:g516428; PIDN:CAA47540.1; PID:g516449  
A:Experimental source: strain India-1967, isolate Ind3  
R:Shchelkunov, S.N.; Blinov, V.M.; Sandakhchiev, L.S. FEBS Lett. 319, 80-83, 1993  
A:Title: Genes of variola and vaccinia viruses necessary to overcome the host protective  
A:Reference number: S32385; MUID:93202281; PMID:8384129  
A:Accession: S32385  
A:Molecule type: DNA  
A:Residues: 31-168 <SHC>  
A:Cross-references: EMBL:X69198  
A:Experimental source: strain India-1967, ssp. major  
C:Genetics:  
A:Gene: G4R  
C:Superfamily: TNF-alpha receptor-II, vaccinia C22L type; NGF receptor repeat homology  
F:32-66/Domain: NGF receptor repeat homology <NGF>  
F:68-109/Domain: NGF receptor repeat homology <NG2>

F:110-151/Domain: NGF receptor repeat homology <NG3>

Query Match 18.5%; Score 210; DB 2; Length 349;  
Best Local Similarity 29.0%; Pred. No. 8.3e-09;  
Matches 45; Conservative 20; Mismatches 80; Indels 10; Gaps 5;

QY 8 PYASENQTRDOEKYEYEPQHRICCSRCPPGTYVS AKSRIRDVTCATCAENSYNHNY 67  
DB 24 PYTPNGKCKDTEYK----RHNLCCLSCPPGTYASRLCDSKTNTQCTPCGSGTFTSRNNH 79  
QY 68 LTICQLCR-PCDPVMGLEIAPCTSKRKTQCRCPGMFC-AAWALECTHCELLSDCPPGT 125  
DB 80 LPACLSNCRGN--SNQVETRSCNTHNRICEPSGYCLLKGGSGCKACVSQTKC--GI 135  
QY 126 EAELEKDEVGKNNHCVPCKAGHFQNTSSPSARCP 160  
DB 136 GYGVSHTSVGDVICSPCGFGTYSHTVSSADKCEP 170

RESULT 13  
D72175  
G2R protein - variola minor virus (strain Garcia-1966)  
C:Species: variola minor virus  
C:Date: 24-Nov-1999 #sequence\_revision 24-Nov-1999 #text\_change 09-Jul-2004  
C:Accession: D72175  
R:Shchelkunov, S.N.; Totnenin, A.V.; Gutorov, V.V.; Safronov, P.F.; Massung, R.F.; Lopar submitted to GenBank, March 1998  
A:Description: Analysis of the complete coding sequence of DNA of alastrim variola minor  
A:Reference number: A72150  
A:Accession: D72175  
A:Status: preliminary  
A:Molecule type: DNA  
A:Residues: 1-349 <SHC>  
A:Cross-references: UNIPROT:P34015; GB:Y16780; NID:g5830555; PIDN:CAB54798.1; PID:g583071  
A:Experimental source: strain Garcia-1966  
C:Genetics:  
A:Gene: G2R  
C:Superfamily: TNF-alpha receptor-II, vaccinia C22L type; NGF receptor repeat homology

Query Match 18.3%; Score 207; DB 2; Length 349;  
Best Local Similarity 29.0%; Pred. No. 1.4e-08;  
Matches 45; Conservative 19; Mismatches 81; Indels 10; Gaps 5;

QY 8 PYASENQTRDOEKYEYEPQHRICCSRCPPGTYVS AKSRIRDVTCATCAENSYNHNY 67  
DB 24 PYTPNGKCKDTEYK----RHNLCCLSCPPGTYASRLCDSKTNTQCTPCGSGTFTSRNNH 79  
QY 68 LTICQLCR-PCDPVMGLEIAPCTSKRKTQCRCPGMFC-AAWALECTHCELLSDCPPGT 125  
DB 80 LPACLSNCRGN--SNQVETRSCNTHNRICEPSGYCLLKGGSGCKACVSQTKC--GI 135  
QY 126 EAELEKDEVGKNNHCVPCKAGHFQNTSSPSARCP 160  
DB 136 GYGVSHTSVGDVICSPCGFGTYSHTVSSADKCEP 170

RESULT 14  
JC4302  
tumor necrosis factor receptor p55 precursor - pig  
C:Species: Sus scrofa domestica (domestic pig)  
C:Date: 29-Nov-1995 #sequence\_revision 08-Feb-1996 #text\_change 09-Jul-2004  
C:Accession: JC4302; PC4093  
R:Suter, B.; Pauli, U. Gene 163, 263-266, 1995  
A:Title: Cloning of the cDNA encoding the porcine p55 tumor necrosis factor receptor.  
A:Reference number: JC4302; MUID:96011645; PMID:7590278  
A:Accession: JC4302  
A:Molecule type: mRNA  
A:Residues: 1-461 <SUT>  
A:Cross-references: UNIPROT:P50555; GB:U19994; NID:gl141752; PIDN:AAC48499.1; PID:gl1417  
A:Accession: PC4093  
A:Molecule type: protein  
A:Residues: 1-7 <SU2>

Query Match	17.7%	Score 201;	DB 2;	Length 277;
Best Local Similarity	28.3%;	Pred. No. 3.3e-08;		
Matches	49; Conservative 21; Mismatches 73; Indels 30; Gaps 5;			
QY	26	POHRIICSRCPCTGYVSAAKSRIRDTVCATCAENSYNEHNHYLTICQLCRPCDPVWGLSEE	85	
Db	37	PSNDRCHCECPGNMGVSRCSRSQNTVCRPGGFYNDVVVSSKP-CKPTCWNLRSGSR	95	
QY	86	IAPCTSRRKTQCRCQPMFCFAAWALEBTHCELLSDCPGTEAELEKDEVGKGNHCVPCKA	145	
Db	96	KOLCTATQDVTCCRAG-----TQPLDSYKPGVD-----CAPCPP	130	
QY	146	GHEFQNTSSPARCQPHTRCENQGLVEAAPGTAQSDTTC--KNPLEPLPPMSG	196	
Db	131	GHP--SPGNOACPKPNTCNCLACKHTLQPASNSSDAICEDRPDPATQPOETQG	181	

Search completed: September 23, 2005, 10:31:19  
Job time : 42 secs

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OM protein - protein search, using sw model

Run on: September 23, 2005, 09:44:31 ; Search time 175 Seconds  
(without alignments)  
576.455 Million cell updates/sec

Title: US-10-077-406-1

Perfect score: 1133

Sequence: 1 SQPQVPPYASENQTCRQDE.....QSDTTCKNPLEPPPMSCGT 197

Scoring table: BLOSUM62

Gapop 10.0 , Gapext 0.5

Searched: 1612378 seqs, 512079187 residues

Total number of hits satisfying chosen parameters: 1612378

Minimum DB seq length: 0

Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%

Maximum Match 100%

Listing first 45 summaries

Database :

Uniprot\_03.\*

1: uniprot\_sprot.\*

2: uniprot\_trembl.\*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

# SUMMARIES

Result No.	Score	Query Match	Length	ID	Description
1	1133	100.0	435	1 TNR3 HUMAN	P36941 homo sapien
2	771	68.0	415	1 TNR3 MOUSE	P50284 mus musculus
3	309.5	27.3	483	1 Q800K7	P20037 paralicthy
4	305	26.9	461	1 TR1B HUMAN	P20333 h tumor nec
5	295.5	26.1	278	2 Q8SQ34	Q8SQ34 sus scrofa
6	295	26.0	474	1 TR1B MOUSE	P25119 mus musculus
7	291.5	25.7	433	2 Q912M6	Q912M6 rattus norv
8	291.5	25.7	461	2 Q6VAU8	Q6VAU8 rattus norv
9	291.5	25.7	474	1 TR1B RAT	Q62327 mus musculus
10	290	25.6	459	2 Q62327	Q62327 mus musculus
11	285.5	25.2	300	1 TR6B HUMAN	Q95407 homo sapien
12	284.5	25.1	274	2 Q7YRL5	Q7YRL5 canis famil
13	283	25.0	625	1 TR11 MOUSE	O35305 mus musculus
14	278	24.5	223	2 Q86YK5	Q86YK5 homo sapien
15	278	24.5	277	1 TNR5 HUMAN	P25942 homo sapien
16	277	24.4	616	1 TR11 HUMAN	Q9Y6G6 homo sapien
17	266.5	23.5	387	2 Q6GLN3	Q6GLN3 xenopus lae
18	265.5	23.4	277	2 Q8WMQ2	Q8WMQ2 ovis aries
19	258	22.8	275	2 Q80WM9	Q80WM9 mus musculus
20	258	22.8	276	2 Q71F55	Q71F55 mus musculus
21	253	22.3	462	2 Q805B0	Q805B0 gallus gall
22	251.5	22.2	269	1 TNR5 BOVIN	Q28203 bos taurus
23	246.5	21.8	401	2 Q6P1I2	Q6P1I2 mus musculus
24	243.5	21.5	289	1 TNR5 MOUSE	P27512 mus musculus
25	243.5	21.5	289	2 Q8K2X6	Q8K2X6 mus musculus
26	242.5	21.4	283	2 Q9XSZ8	Q9XSZ8 cercopithec
27	242.5	21.4	401	1 T11B MOUSE	Q08712 mus musculus
28	240	21.2	186	2 Q727J5	Q727J5 cowpox viru
29	239.5	21.1	401	1 T11B HUMAN	O00300 homo sapien
30	238.5	21.1	318	2 Q7T2H3	Q7T2H3 oncorhynch
31	238	21.0	302	2 Q9PUS0	Q9PUS0 salvelinus

32	235.5	20.8	401	1 T11B RAT	O08727 rattus norv
33	233.5	20.6	457	2 Q8IVS6	Q8IVS6 homo sapien
34	232.5	20.5	467	2 Q800I0	Q800I0 gallus gall
35	232	20.5	270	2 Q7SSV8	Q7SSV8 felis silve
36	230.5	20.3	283	1 TR14 HUMAN	Q92956 homo sapien
37	230	20.3	276	2 Q9DDD2	Q9DDD2 gallus gall
38	230	20.3	351	2 Q57117	Q57117 cowpox viru
39	229.5	20.3	285	2 Q90W71	Q90W71 oncorhynch
40	228.5	20.2	655	1 TR21 HUMAN	O75509 homo sapien
41	226.5	20.0	167	2 Q8UYL3	Q8UYL3 vaccinia vi
42	226.5	20.0	655	1 TR21 MOUSE	Q9EPUS mus musculu
43	225.5	19.9	186	2 Q7ZZY5	Q7ZZY5 gallus gall
44	225.5	19.9	651	2 Q98SM6	Q98SM6 gallus gall
45	225	19.9	186	2 Q9YP87	Q9YP87 cowpox viru

## ALIGNMENTS

RESULT 1  
ID TNR3 HUMAN STANDARD; PRT; 435 AA.  
AC P36941;  
DT 01-JUN-1994 (Rel. 29, Created)  
DT 01-JUN-1994 (Rel. 29, Last sequence update)  
DT 05-JUL-2004 (Rel. 44, Last annotation update)  
DE Tumor necrosis factor receptor superfamily member 3 precursor  
DE (Lymphotoxin-beta receptor) (Tumor necrosis factor receptor 2 related  
DE protein) (Tumor necrosis factor C receptor).  
GN Name=LTR; Synonyms=TNFRC, TNFRSF3;  
OS Homo sapiens (Human).  
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;  
OC Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.  
OX NCBI\_TaxID=9606;  
RN [1]  
RP SEQUENCE FROM N.A.  
RC TISSUE=Liver;  
RX MEDLINE=93252381; PubMed=8486360;  
RA Baens M., Chaffanet M., Cassiman J.J., den Berghe H., Marynen P.;  
RT "Construction and evaluation of a hncDNA library of human 12p  
transcribed sequences derived from a somatic cell hybrid."  
RL Genomics 16:214-218(1993);  
[2]  
RP SEQUENCE FROM N.A.  
RC TISSUE=lung;  
RX MEDLINE=22388257; PubMed=12477932; DOI=10.1073/pnas.242603899;  
RA Strausberg R.L., Feingold E.A., Grouse L.H., Derge J.G.,  
Klausner R.D., Collins F.S., Wagner L., Shenmen C.M., Schuler G.D.,  
Altschul S.F., Zeeberg B., Buetow K.H., Schaefer C.F., Bhat N.K.,  
Hopkins R.F., Jordan H., Moore T., Max S.I., Wang J., Hsieh F.,  
Diatchenko L., Marusina K., Farmer A.A., Rubin G.M., Hong L.,  
Stapleton M., Soares M.B., Bonaldo M.F., Casavant T.L., Schetz T.E.,  
Brownstein M.J., Ussin T.B., Toshiyuki S., Carninci P., Prange C.,  
Raha S.S., Loquellano N.A., Peters G.J., Abramson R.D., Mullahy S.J.,  
Bosak S.A., McKernan K.J., Malek J.A., Guntarat P.H.,  
Richards S., Worley K.C., Hale S., Garcia A.M., Gay L.J., Hulyk S.W.,  
Villalon D.K., Muzny D.M., Sodergren E.J., Lu X., Gibbs R.A.,  
Fahey J., Hellon E., Kettman M., Madan A., Rodrigues S., Sanchez A.,  
Whiting M., Madan A., Young A.C., Shevchenko Y., Bouffard G.G.,  
Blakesley R.W., Touchman J.W., Green E.D., Dickinson M.C.,  
Rodriguez A.C., Grimwood J., Schmutz J., Myers R.M.,  
Butterfield Y.S.N., Krzywinski M.I., Skalska U., Smalls D.E.,  
Schnerch A., Schein J.E., Jones S.J.M., Marra M.A.;  
RT "Generation and initial analysis of more than 15,000 full-length human  
and mouse cDNA sequences."  
Proc. Natl. Acad. Sci. U.S.A. 99:16999-16903(2002)  
[3]  
RP FUNCTION.  
RX MEDLINE=94225209; PubMed=8171323;  
RA Crowe P.D., VanArsdale T.L., Walter B.N., Ware C.F., Hession C.,  
Ehrenfels B., Browning J.L., Din W.S., Goodwin R.G., Smith C.A.;  
RT "A lymphotoxin-beta-specific receptor."  
Science 264:707-710(1994).

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RN RP CHARACTERIZATION.
RX MEDLINE=99223511; PubMed=10207006; DOI=10.1074/jbc.274.17.11868;
RA Wu M.-Y., Wang P.-Y., Han S.-H., Heieh S.-L.;
RT "The cytoplasmic domain of the lymphotoxin-beta receptor mediates cell
RL death in HeLa cells.";
RN J. Biol. Chem. 274:11868-11873(1999).
RN [5]
RN FUNCTION.
RP MEDLINE=20261554; PubMed=10799510; DOI=10.1074/jbc.275.19.14307;
RX Rooney I.A., Butrovich K.D., Glass A.A., Borboroglu S., Benedict C.A.,
RA Nakano H., Okumura H., Chung W., Williams-Abbott L., Ware C.F.,
RA Whitebeck J.C., Cohen G.H., Eisenberg R.J., Ware C.F.;
RT "The lymphotoxin-beta receptor is necessary and sufficient for LIGHT-
RT mediated apoptosis of tumor cells.";
RN J. Biol. Chem. 275:14307-14315(2000).
RN [6]
RN INTERACTION WITH TRAF3.
RP MEDLINE=96278943; PubMed=8663299; DOI=10.1074/jbc.271.25.14661;
RX Nakano H., Okumura H., Chung W., Williams-Abbott L., Ware C.F.,
RA Yagita H., Okumura K.;
RA "TRAF5, an activator of NF-kappaB and putative signal transducer for
RT the lymphotoxin-beta receptor.";
RL J. Biol. Chem. 271:14661-14664(1996).
RN [7]
RN INTERACTION WITH TRAF4.
RP MEDLINE=98289299; PubMed=9626059;
RX Krajewska M., Krajewski S., Zapata J.M., VanArsdale T., Gascoyne R.D.,
RA Berern K., McFadden D., Shabaik A., Hugh J., Reynolds A.,
RA Clevenger C.V., Reed J.C.;
RT "TRAF-4 expression in epithelial progenitor cells. Analysis in normal
RT adult, fetal, and tumor tissues.";
RL Am. J. Pathol. 152:1549-1561(1998).
RN [8]
RN INTERACTION WITH TRAF5.
RP MEDLINE=98172745; PubMed=9511754; DOI=10.1016/S0378-1119(97)00616-1;
RX Mizushima S.-I., Fujita M., Ishida T., Azuma S., Kato K., Hirai M.,
RA Otsuka M., Yamamoto T., Inoue J.-I.;
RT "Cloning and characterization of a cDNA encoding the human homolog of
RT tumor necrosis factor receptor-associated factor 5 (TRAF5).";
RL Gene 207:135-140(1998).
RN CC -!- FUNCTION: Receptor for the heterotrimeric lymphotoxin containing
CC LTA and LTb, and for TNFSF14/LIGHT. Promotes apoptosis via TRAF3
CC and TRAF5. May play a role in the development of lymphoid organs.
CC -!- SUBUNIT: Self-associates. Associates with TRAF3, TRAF4 and TRAF5.
CC -!- SUBCELLULAR LOCATION: Type I membrane protein.
CC -!- SIMILARITY: Contains 4 TNFR-Cys repeats.
CC -----
CC This SWISS-PROT entry is copyright. It is produced through a collaboration
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CC -----
CC EMBL; L04270; AAA36757.1; -.
CC EMBL; BC026262; AAH26262.1; -.
CC F01; 154182; I54182.
CC HSP; Q92956; IJMA.
CC Genew; HGNC:6718; LTBR.
CC H-InvDB; HIX0010362; -.
CC MIM; 600979; -.
CC GO; GO:0005515; F:protein binding; IPI.
CC GO; GO:0004871; F:signal transducer activity; IBP.
CC GO; GO:0043123; P:positive regulation of I-kappaB kinase/NF-k. .; IEP.
CC GO; GO:0007165; P:signal transduction; TAS.
CC InterPro; IPR008063; Fas receptor.
CC InterPro; IPR001368; TNFR_c6.
CC Pfam; PF00020; TNFR_c6; 4.
CC PRINTS; PR01680; FASRECEPTOR.
CC SMART; SM00208; TNFR; 4.
CC PROSITE; PS00652; TNFR_NGFR_1; 2.
CC PROSITE; PS00500; TNFR_NGFR_2; 3.

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KW Apoptosis; Glycoprotein; Receptor; Repeat; Signal; Transmembrane.
FT SIGNAL 1 30 Potential.
FT CHAIN 31 435 tumor necrosis factor receptor
FT TRANSMEM 228 247 superfamilly member 3.
FT DOMAIN 31 227 Extracellular (Potential).
FT TRANSMEM 228 247 Potential.
FT DOMAIN 249 435 Cytoplasmic (Potential).
FT REPEAT 42 81 TNFR-Cys 1.
FT REPEAT 82 124 TNFR-Cys 2.
FT REPEAT 125 168 TNFR-Cys 3.
FT REPEAT 169 211 TNFR-Cys 4.
FT DISULFID 43 58 By similarity.
FT DISULFID 59 72 By similarity.
FT DISULFID 62 80 By similarity.
FT DISULFID 83 98 By similarity.
FT DISULFID 101 116 By similarity.
FT DISULFID 104 124 By similarity.
FT DISULFID 126 132 By similarity.
FT DISULFID 139 148 By similarity.
FT DISULFID 142 167 By similarity.
FT DISULFID 170 185 By similarity.
FT CARBOHYD 40 40 N-linked (GlcNAc..) (Potential).
FT CARBOHYD 177 177 N-linked (GlcNAc..) (Potential).
SQ SEQUENCE 435 AA; 46709 MW; 624626E6022F656F CRC64;

Query Match 100.0%; Score 1133; DB 1; Length 435;
Best Local Similarity 100.0%; Pred. No. 9.1e-88;
Matches 197; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 SQQAVPPYASENOTCRDQEKYEYEPQHRICCSRCPPGTYVSAKSRIKDTVCATCAENS 60
DB 28 SQQAVPPYASENQTCRDQEKYEYEPQHRICCSRCPPGTYVSAKSRIKDTVCATCAENS 87
QY 61 YNEHWNYLTICQLCRPCDPVNGLEBIAPTSKRTQCRQCPGMFCAAWALECTHCELLSD 120
DB 88 YNEHWNYLTICQLCRPCDPVNGLEBIAPTSKRTQCRQCPGMFCAAWALECTHCELLSD 147
QY 121 CPPTGEALKEDEVGKNNHCVPCKAGHFQNTSSPSARCOPHTRCENQGLVEAAPGTAQSD 180
DB 148 CPPTGEALKEDEVGKNNHCVPCKAGHFQNTSSPSARCOPHTRCENQGLVEAAPGTAQSD 207
QY 181 TTCKNPLEPLPPMSGT 197
DB 208 TTCKNPLEPLPPMSGT 224

RESULT 2
TNR3_MOUSE
ID TNR3_MOUSE STANDARD; PRT; 415 AA.
AC P50284;
DT 01-OCT-1996 (Rel. 34, Created)
DT 01-OCT-1996 (Rel. 34, Last sequence update)
DT 05-JUL-2004 (Rel. 44, Last annotation update)
DE Tumor necrosis factor receptor superfamily member 3 precursor
DE (Lymphotoxin-beta receptor).
DE Name=Icbr; Synonyms=TNFR, Tnfrsf3;
DE Mus musculus (Mouse).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
OX NCBI_TaxID=10090;
RN [1]_
RP SEQUENCE FROM N.A.
RC STRAIN=CVB; TISSUE=Lung;
RX MEDLINE=96072804; PubMed=7594541;
RA Force W.R., Walter B.N., Hession C., Tizard R., Kozak C.A.,
RA Browning J.L., Ware C.F.;
RT "Mouse lymphotoxin-beta receptor. Molecular genetics, ligand binding,
RT and expression."
RL J. Immunol. 155:5280-5288(1995).
RN [2]
RN SEQUENCE FROM N.A.
RX MEDLINE=96163885; PubMed=8586432;
RA Nakamura T., Tashiro K., Nazarea M., Nakano T., Sasayama S., Honjo T.;

```



RT "The murine lymphotoxin-beta receptor cDNA: isolation by the signal  
sequence trap and chromosomal mapping.";  
RL Genomics 30:312-319(1995).  
RN [3]  
RC INTERACTION WITH TRAF5.  
RX STRAIN=BALB/C;  
RA MEDLINE=96278943; PubMed=8663299; DOI=10.1074/jbc.271.25.14661;  
RA Nakano H., Oshima H., Chung W., Williams-Abbott L., Ware C.F.,  
RA Yagita H., Okumura K.;  
RT "TRAF5, an activator of NF-kappaB and putative signal transducer for  
the lymphotoxin-beta receptor.";  
RL J. Biol. Chem. 271:14661-14664(1996).  
CC -!- FUNCTION: Receptor for the heterotrimeric lymphotoxin containing  
LTA and LTB, and for TNFSF14/LIGHT. Promotes apoptosis via TRAF3  
and TRAF5. May play a role in the development of lymphoid organs  
(By similarity).  
CC -!- SUBUNIT: Self-associates (By similarity). Associates with TRAF5.  
CC Associates with TRAF3 and TRAF4 (By similarity).  
CC -!- SUBCELLULAR LOCATION: Type I membrane protein.  
CC -!- SIMILARITY: Contains 4 TNFR-Cys repeats.  
CC -----  
CC This SWISS-PROT entry is copyright. It is produced through a collaboration  
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CC -----  
DR EMBL; U29173; AAC68964.1; -;  
DR EMBL; L38423; AAB00846.1; -;  
DR EMBL; U30798; AAB81334.1; -;  
DR HSSP; O14763; LDU3  
DR MGD; MGI:104875; Ltblr.  
DR InterPro; IPR001368; TNFR\_C6.  
DR Pfam; PF00020; TNFR\_C6; 3.  
DR SMART; SM00208; TNFR; 3.  
DR PROSITE; PS00652; TNFR\_NGFR\_1; 2.  
DR PROSITE; PS00050; TNFR\_NGFR\_2; 3.  
KW Apoptosis; Glycoprotein; Receptor; Repeat; Signal; Transmembrane.  
FT SIGNAL 1 30 Potential.  
FT CHAIN 31 415 Tumor necrosis factor receptor  
FT DOMAIN 31 223 Extracellular member 3.  
FT TRANSMEM 224 244 Potential.  
FT DOMAIN 245 415 Potential.  
FT REPEAT 42 81 Cytoplasmic (Potential).  
FT REPEAT 82 124 TNFR-Cys 1.  
FT REPEAT 125 170 TNFR-Cys 2.  
FT REPEAT 171 213 TNFR-Cys 3.  
FT REPEAT 214 257 TNFR-Cys 4.  
FT DISULFID 43 58 By similarity.  
FT DISULFID 59 72 By similarity.  
FT DISULFID 62 80 By similarity.  
FT DISULFID 83 98 By similarity.  
FT DISULFID 101 116 By similarity.  
FT DISULFID 104 124 By similarity.  
FT DISULFID 126 132 By similarity.  
FT DISULFID 139 150 By similarity.  
FT DISULFID 142 169 By similarity.  
FT DISULFID 172 187 By similarity.  
FT CARBOHYD 40 40 N-linked (GlcNAc...) (Potential).  
FT CARBOHYD 179 179 N-linked (GlcNAc...) (Potential).  
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Best Local Similarity 70.7%; Pred. No. 3.5e-57;  
Matches 135; Conservative 14; Mismatches 40; Indels 2; Gaps 1;  
QY 1 SQPQAVPPVASENOTCRDQKEYEYEPQHRICCSRCPPGTVVSAKCSRIKDTVCATCAENS 60  
DB 28 SQPQLVPPYRIENQTCWDQDKEYEYEPMDVCCSRCPGFEVFAVCSRSQDTVCKTCPHNS 87  
QY 61 YNEHWNLYITCQLCRPCDIPVMGLEETAPCTSKRKTQCRCPQGMFCAAWALECTHC--ELL 118

DB 88 YNEHWNHLSCTQLCRPCDIPVMGLEETAPCTSKRKAECRCQPGMSCVYLDNECVHCBEERL 147  
QY 119 SDCPPGTEAEALKDEVGKGNHCVPCAKGHFQNTSSPSARCPQHTRCENOGLYEAPAGTAQ 178  
DB 148 VLCQGTGTEAEVTDIMTDVNCVPCPGHFGHNTSSPRARCPQHTRCCEIQGLVEAAPGTSY 207  
QY 179 SDTCKKNPLEP 189  
DB 208 SDTICKNPPPEP 218  
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Q800K7 PRELIMINARY; PRT; 483 AA.  
AC Q800K7;  
DT 01-JUN-2003 (TRENBLrel. 24, Created)  
DT 01-JUN-2003 (TRENBLrel. 24, Last sequence update)  
DT 01-MAR-2004 (TRENBLrel. 26, Last annotation update)  
DE Tumor necrosis factor receptor-2.  
GN Name=TNFR-2;  
OS Paracitichthys olivaceus (Japanese flounder).  
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;  
OC Actinopterygii; Neopterygii; Teleostei; Euteleostei; Neoteleostei;  
OC Acanthomorpha; Acanthopterygii; Percomorpha; Pleuronectiformes;  
OC Pleuronectoidae; Paracitichthyidae; Paracitichthys.  
OX NCBI\_TaxID=8255;  
RN [1]  
RP SEQUENCE FROM N.A.  
RX MEDLINE=22518447; PubMed=12631519; DOI=10.1016/S0145-305X(02)00118-0;  
RT Park C., Kurobe T., Hirono I., Aoki T.;  
RT "Cloning and characterization of cDNAs for two distinct tumor necrosis  
factor receptor superfamily genes from Japanese flounder Paracitichthys  
RT olivaceus";  
RL Dev. Comp. Immunol. 27:365-375(2003).  
DR EMBL; AB080947; BAC65226.1; -;  
DR HSSP; Q92956; 1JWA.  
DR GO; GO:0016021; C:integral to membrane; IEA.  
DR GO; GO:0004872; F:receptor activity; IEA.  
DR GO; GO:0005031; F:tumor necrosis factor receptor activity; IEA.  
DR GO; GO:0019221; P:cytokine and chemokine mediated signaling p...; IEA.  
DR InterPro; IPR011366; TNFR\_2.  
DR InterPro; IPR001368; TNFR\_C6.  
DR Pfam; PF00020; TNFR\_C6; 2.  
DR PIRSF; PIRSF001968; TNFR\_2; 1.  
DR SMART; SM00208; TNFR; 4.  
DR PROSITE; PS00652; TNFR\_NGFR\_1; UNKNOWN\_1.  
DR PROSITE; PS00050; TNFR\_NGFR\_2; 3.  
KW Receptor.  
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Query Match 27.3%; Score 309.5; DB 2; Length 483;  
Best Local Similarity 35.4%; Pred. No. 4.3e-18;  
Matches 64; Conservative 20; Mismatches 80; Indels 17; Gaps 6;  
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DB 27 CHNSTTETREQD--LCCKKCPGQRLIQKCSATESVKQCSGGYMEKNTAQKCLSCN 84  
QY 76 PCDPVMGLEETAPCTSKRKTQCRCPQGMFCAAWALE-----CTHCELLSDCPPGTEAEALK 130  
DB 85 KCKSNKGLQYACQRCSTTRTGCVCKPGMYC---IMDFPNYCAECRNTSQCRAGYGVSLP 141  
QY 131 DEVGKGN--HCVPCAKGHFQNTSSPSARCPQHTRCENOGLYEAPAGTAQSDTCKNPLE 188  
DB 142 ---GKNSDVKCELCPDGMFNSNTSTTETCRPHTDCHGKAVR--KGNTTSDTVCBEVGA 196  
QY 189 P 189  
DB 197 P 197  
RESULT 4

TRIBL HUMAN  
 ID TRIBL\_HUMAN STANDARD; PRT; 461 AA.  
 AC P20333; Q16042; Q6Y129; Q9U1H1;  
 DT 01-FEB-1991 (Rel. 17, Created)  
 DT 28-FEB-2003 (Rel. 41, Last sequence update)  
 DT 25-JAN-2005 (Rel. 46, Last annotation update)  
 DE Tumor necrosis factor receptor superfamily member 1B precursor (Tumor  
 DE necrosis factor receptor 2) (TNF-R2) (tumor necrosis factor receptor  
 DE type II) (p75) (p80 TNF-alpha receptor) (CD120b) (Etanercept)  
 DE [Contains: Tumor necrosis factor binding protein 2 (TNFRII) (TNF-2)].  
 GN Name:TNFRSF1B; Synonyms:TNFR, TNFR2;  
 OS Homo sapiens (Human)  
 OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;  
 OC Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.  
 OX NCBI\_TaxID=9606;  
 RN [1]  
 RP SEQUENCE FROM N.A. (ISOFORM 1).  
 RX MEDLINE=90260639; PubMed=2160731;  
 RA Smith C.A., Davis T., Anderson D., Solam L., Beckmann M.P., Jerzy R.,  
 RA Dower S.K., Cosman D., Goodwin R.G.;  
 RT "A receptor for tumor necrosis factor defines an unusual family of  
 RT cellular and viral proteins.";  
 RL Science 248:1019-1023(1990).  
 RN [2]  
 RP SEQUENCE FROM N.A. (ISOFORM 1), AND VARIANT ARG-196.  
 RX MEDLINE=91045991; PubMed=2172983;  
 RA Kohno T., Brewer M.T., Baker S.L., Schwartz P.E., King M.W.,  
 RA Hale K.K., Squires C.H., Thompson R.C., Vannice J.L.;  
 RT "A second tumor necrosis factor receptor gene product can shed a  
 RT naturally occurring tumor necrosis factor inhibitor.";  
 RL Proc. Natl. Acad. Sci. U.S.A. 87:8331-8335(1990).  
 RN [3]  
 RP SEQUENCE FROM N.A. (ISOFORM 1).  
 RX MEDLINE=96299745; PubMed=8661109; DOI=10.1006/geno.1996.0327;  
 RA Beltinger C.P., White P.S., Maris J.M., Sulman E.P., Jensen S.J.,  
 RA Lepaslier D., Stallard B.J., Goeddel D.V., Desauvage F.J.,  
 RA Brodeur G.M.;  
 RT "Physical mapping and genomic structure of the human TNFR2 gene.";  
 RL Genomics 35:194-100(1996).  
 RN [4]  
 RP SEQUENCE FROM N.A. (ISOFORM 2), SUBCELLULAR LOCATION, AND FUNCTION OF  
 RP ISOFORM 2.  
 RX PubMed=14688072; DOI=10.1093/intimm/dxh014;  
 RA Lainez B., Fernandez-Real J.M., Romero X., Esplugues E., Canete J.D.,  
 RA Ricart W., Engel P.;  
 RT "Identification and characterization of a novel spliced variant that  
 RT encodes human soluble tumor necrosis factor receptor 2.";  
 RL Int. Immunol. 16:169-177(2004).  
 RN [5]  
 RP SEQUENCE FROM N.A., AND VARIANTS MET-187; ARG-196; LYS-232; THR-236;  
 RP PRO-264 AND ARG-295.  
 RA Rieder M.J., Livingston R.J., Daniels M.R., Chung M.-W.,  
 RA Miyamoto K.E., Nguyen C.P., Nguyen D.A., Poel C.L., Robertson P.D.,  
 RA Schackwitz W.S., Sherwood J.K., Witrak L.A., Nickerson D.A.,  
 RT "NIHES-SNPs, environmental genome project, NIHES ES15478, Department  
 RT of Genome Sciences, Seattle, WA (URL: http://pgp.gs.washington.edu).";  
 RL Submitted (MAR-2003) to the EMBL/GenBank/DBJ databases.  
 RN [6]  
 RP SEQUENCE FROM N.A., AND VARIANTS ARG-196; LYS-232; PRO-269 AND  
 RP ARG-301.  
 RA Rieder M.J., Carrington D.P., da Ponte S.H., Hastings N.C.,  
 RA Ahearn M.O., Kuldane K.S., Rajkumar N., Toth E.J., Yi Q.,  
 RA Nickerson D.A.;  
 RT "SeattleSNPs, NHLBI HL6682 program for genomic applications, UW-  
 RT FHCRC, Seattle, WA (URL: http://pga.gs.washington.edu).";  
 RL Submitted (JUL-2003) to the EMBL/GenBank/DBJ databases.  
 RN [7]  
 RP SEQUENCE FROM N.A. (ISOFORM 1).  
 RC TISSUE=ENS;  
 RX MEDLINE=22388257; PubMed=12477932; DOI=10.1073/pnas.242603899;  
 RA Strausberg R.L., Feingold E.A., Grouse L.H., Derge J.G.,  
 RA Klausner R.D., Collins F.S., Wagner L., Shenmen C.M., Schuler G.D.,  
 RA Altschul S.F., Zeeberg B., Buetow K.H., Schaefer C.F., Bhat N.K.,

RA Hopkins R.F., Jordan H., Moore T., Max S.I., Wang J., Hsieh F.,  
 RA Diatchenko L., Marusina K., Farmer A.A., Rubin G.M., Hong L.,  
 RA Stapleton M., Soares M.B., Bonaldo M.F., Casavant T.L., Scheetz T.E.,  
 RA Brownstein M.J., Usdin T.B., Toshiyuki S., Carninci P., Prange C.,  
 RA Raha S.S., Loquellano N.A., Peters G.J., Abramson R.D., Mullaby S.J.,  
 RA Bosak S.A., McEwan P.J., McKernan K.J., Malek J.A., Gunaratne P.H.,  
 RA Richards S., Worley K.C., Hale S., Garcia A.M., Gay L.J., Hulyk S.W.,  
 RA Villalon D.K., Muzny D.M., Sodergren E.J., Lu X., Gibbs R.A.,  
 RA Fahey J., Helton E., Kettman M., Madan A., Rodrigues S., Sanchez A.,  
 RA Whiting M., Madan A., Young A.C., Shevchenko Y., Bouffard G.G.,  
 RA Blakesley R.W., Touchman J.W., Green E.D., Dickson M.C.,  
 RA Rodriguez A.C., Grimwood J., Schmutz J., Myers R.M.,  
 RA Butterfield Y.S.N., Krzywinski M.I., Skalska U., Smailus D.E.,  
 RA Schnerch A., Schein J.E., Jones S.J.M., Marra M.A.;  
 RT "Generation and initial analysis of more than 15,000 full-length human  
 RT and mouse cDNA sequences.";  
 RL Proc. Natl. Acad. Sci. U.S.A. 99:16899-16903(2002).  
 RN [8]  
 RP SEQUENCE OF 37-461 FROM N.A. (ISOFORM 1).  
 RX MEDLINE=91370690; PubMed=1966549; DOI=10.1016/1043-4666(90)90022-L;  
 RA Dembic Z., Loetscher H., Gubler U., Pan Y.C., Lahm H.-W., Gentz R.,  
 RA Brockhaus M., Lesslauer W.;  
 RT "Two human TNF receptors have similar extracellular, but distinct  
 RT intracellular, domain sequences.";  
 RL Cytokine 2:231-237(1990).  
 RN [9]  
 RP SEQUENCE OF 116-461 FROM N.A. (ISOFORM 1), PARTIAL SEQUENCE, AND  
 RP VARIANT ARG-196.  
 RX MEDLINE=90349572; PubMed=2166946;  
 RA Heller R.A., Song K., Onasch M.A., Fischer W.H., Chang D.,  
 RA Ringold G.M.;  
 RT "Complementary DNA cloning of a receptor for tumor necrosis factor and  
 RT demonstration of a shed form of the receptor.";  
 RL Proc. Natl. Acad. Sci. U.S.A. 87:6151-6155(1990).  
 RN [10]  
 RP SEQUENCE OF 154-183 FROM N.A., AND VARIANTS ARG-196 AND LYS-232.  
 RX MEDLINE=21069356; PubMed=11197692; DOI=10.1038/sj.gene.6363700;  
 RA Tsuchiya N., Komata T., Matsushita M., Ohashi J., Tokunaga K.;  
 RT "New single nucleotide polymorphisms in the coding region of human  
 RT TNFR2: association with systemic lupus erythematosus.";  
 RL Genes Immun. 1:501-503(2000).  
 RN [11]  
 RP SEQUENCE OF 27-33.  
 RC TISSUE=Urine;  
 RX MEDLINE=90110215; PubMed=2153136;  
 RA Engelmann H., Novick D., Wallach D.;  
 RT "Two tumor necrosis factor-binding proteins purified from human urine.  
 RT Evidence for immunological cross-reactivity with cell surface tumor  
 RT necrosis factor receptors.";  
 RL J. Biol. Chem. 265:1531-1536(1990).  
 RN [12]  
 RP SEQUENCE OF 23-40; 65-69; 136-141; 300-306 AND 346-362.  
 RX MEDLINE=91056048; PubMed=2173696;  
 RA Loetscher H., Schlaeger E.J., Lahm H.-W., Pan Y.-C.E., Lesslauer W.,  
 RA Brockhaus M.;  
 RT "Purification and partial amino acid sequence analysis of two distinct  
 RT tumor necrosis factor receptors from HL60 cells.";  
 RL J. Biol. Chem. 265:20131-20138(1990).  
 RN [13]  
 RP CHARACTERIZATION.  
 RX MEDLINE=93016040; PubMed=1328224;  
 RA Pennica D., Lam V.T., Mize N.K., Weber R.F., Lewis M., Fendly B.M.,  
 RA Lipari M.T., Goeddel D.V.;  
 RT "Biochemical properties of the 75-kDa tumor necrosis factor receptor.  
 RT Characterization of ligand binding, internalization, and receptor  
 RT phosphorylation.";  
 RL J. Biol. Chem. 267:21172-21178(1992).  
 RN [14]  
 RP INTERACTION WITH TRAF2.  
 RX MEDLINE=94349371; PubMed=8069916; DOI=10.1016/0092-8674(94)90532-0;  
 RA Rothe M., Wong S.C., Henzel W.J., Goeddel D.V.;  
 RT "A novel family of putative signal transducers associated with the  
 RT cytoplasmic domain of the 75 kDa tumor necrosis factor receptor.";

Db 192 GNASMDAVCTSTSPTRSMAP 211

RESULT 5

Q8SQ34 PRELIMINARY; PRT; 278 AA.

ID Q8SQ34 AC Q8SQ34

DT 01-JUN-2002 (TrEMBLrel. 21, Created)

DT 01-JUN-2002 (TrEMBLrel. 21, Last sequence update)

DT 01-JUN-2003 (TrEMBLrel. 24, Last annotation update)

DE CD40.

OS Sus scrofa (Pig).

OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;

OC Mammalia; Eutheria; Chetartiodactyla; Suina; Suidae; Sus.

OX NCBI\_TaxID=9823;

RN [1]

RP SEQUENCE FROM N.A.

RA West K.A., Li A.W., Rowden G.;

RL Submitted (MAR-2000) to the EMBL/GenBank/DBJ databases.

RR EMBL; AF248545; AAL92924.1; -

DR HSSP; P25942; IFLN.

DR GO; GO:0016020; C:membrane; IEA.

DR GO; GO:0004888; F:transmembrane receptor activity; IEA.

DR GO; GO:0006915; P:apoptosis; IEA.

DR GO; GO:0006955; P:immune response; IEA.

DR GO; GO:0007165; P:signal transduction; IEA.

DR InterPro; IPR008063; Fas receptor.

DR InterPro; IPR001368; TNFR\_c6.

DR Pfam; PF00020; TNFR\_c6; 1.

DR PRINTS; PR01680; FASRECEPTOR.

DR SMART; SM00208; TNFR; 4.

DR PROSITE; PS00652; TNFR\_NGFR\_1; 1.

DR PROSITE; PS50050; TNFR\_NGFR\_2; 4.

DR SEQUENCE 278 AA; 30951 MW; 20D446E44AP93DD2 CRC64;

Query Match 26.1%; Score 295.5; DB 2; Length 278;

Best Local Similarity 36.9%; Pred. No. 3.8e-17;

Matches 62; Conservative 19; Mismatches 74; Indels 13; Gaps 3

Qy 21 KEYVEQHRICCSRCPPGTVSACSRIRTVCACTCAENSYNEHWNYLTICQLCRCPDPV 80

Db 27 KENQYPTNSRCNCLPPGQGLVNHCTEVTETELPCSSSEFLATWNRKHKCHQHKYCDPN 86

Qy 81 MGLEETAPCTSKRKTCCRCQCPGMFCAAWALECTHCELLSDCPPG-----TEAEIKDEVGK 135

Db 87 LGHQVQREGTSKTDTCVCSEGHHTNSA--CRSCTLHSLCFPGGLGVQKQMATREVSDTI-- 142

Qy 136 GNNHCVPCKAGHFQNTSSPSARCQPHTRCENQGLVEAAPGTAQSDTTTC 183

Db 143 ----CEPCPGVGFNSVSSASEKQPWTSCESKGLVQERAGTNKTDVVC 186

RESULT 6

ID TRIB\_MOUSE STANDARD; PRT; 474 AA.

AC P25119; O88734; P97893;

DT 01-MAY-1992 (Rel. 22, Created)

DT 01-MAY-1992 (Rel. 22, Last sequence update)

DT 25-JAN-2005 (Rel. 46, Last annotation update)

DE Tumor necrosis factor receptor superfamily member 1B precursor (Tumor

DE necrosis factor receptor 2) (TNF-R2) (Tumor necrosis factor receptor

DE type II) (p75) (p80 TNF-alpha receptor).

GN Name=TNfrsf1b; Synonyms=tnfr-2, Tnfr2;

OS Mus musculus (Mouse).

OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;

OC Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.

OX NCBI\_TaxID=10090;

RN [1]

RP SEQUENCE FROM N.A.

RX MEDLINE=91187885; PubMed=1849278;

RA Lewis M., Tartaglia L.A., Lee A., Bennett G.L., Rice G.C., Wong G.H.,

RA Chen E.Y., Goeddel D.V.;

"Cloning and expression of cDNAs for two distinct murine tumor necrosis factor receptors demonstrate one receptor is species specific.";  
 RL Proc. Natl. Acad. Sci. U.S.A. 88:2830-2834(1991).  
 [2]  
 RN SEQUENCE FROM N.A.  
 RX MEDLINE=91246168; PubMed=1645445;  
 RA Goodwin R.G., Anderson D., Jerzy R., Davis T., Brannan C.I., Copeland N.G., Jenkins N.A., Smith C.A.;  
 RA "Molecular cloning and expression of the type 1 and type 2 murine TNF receptors for tumor necrosis factor.";  
 RT Mol. Cell. Biol. 11:3020-3026(1991).  
 RN [3].  
 RN SEQUENCE FROM N.A.  
 RX MEDLINE=98414512; PubMed=9740674; DOI=10.1006/geno.1998.5407;  
 RA Hurlle B., Segade F., Rodriguez R., Ramos S.S., Lazo P.S.;  
 RA "The mouse tumor necrosis factor receptor 2 gene: genomic structure and characterization of the two transcripts.";  
 RT Genomics 52:79-98(1998).  
 RN [4].  
 RN SEQUENCE OF 1-26 FROM N.A.  
 RC STRAIN=NOD;  
 RA Jacob C.O., Liu J.;  
 RA Submitted (JAN-1996) to the EMBL/GenBank/DBJ databases.  
 RN [5].  
 RN SEQUENCE OF 1-22 FROM N.A.  
 RC TISSUE=Liver;  
 RA Kissingerghis M., Fellowes R., Feldmann M., Chernajovsky Y.;  
 RA Submitted (MAY-1995) to the EMBL/GenBank/DBJ databases.  
 CC -!- FUNCTION: Receptor with high affinity for TNFSF2/TNFR-alpha and approximately 5-fold lower affinity for homotrimeric TNFSF1/lymphotoxin-alpha. the TRAF1/TRA2 complex recruits the apoptotic suppressors BIRC2 and BIRC3 to TNFSF1B/TNFR2 (By similarity).  
 CC -!- SUBUNIT: Binds to TRAF2 (By similarity).  
 CC -!- SUBCELLULAR LOCATION: Type I membrane protein.  
 CC -!- SIMILARITY: Contains 4 TNFR-Cys repeats.  
 CC -----  
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 CC -----  
 DR EMBL; M60469; AAA39752.1; -;  
 DR EMBL; M59378; AAA40463.1; -;  
 DR EMBL; Y14619; CAA74969.1; -;  
 DR EMBL; Y14620; CAA74969.1; JOINED.  
 DR EMBL; Y14621; CAA74969.1; JOINED.  
 DR EMBL; Y14622; CAA74969.1; JOINED.  
 DR EMBL; Y14623; CAA74969.1; JOINED.  
 DR EMBL; U39488; AAB85021.1; -;  
 DR EMBL; X87128; CAA60618.1; -;  
 DR FIR; B38634; B38634.  
 DR HSSP; P19438; INCF.  
 DR MGD; MGI:1314883; Tnfrsf1b.  
 DR GO; GO:0007166; P:cell surface receptor linked signal transdu. . .; IMP.  
 DR GO; GO:0006954; P:inflammatory response; IMP.  
 DR GO; GO:0008220; P:necrosis; IMP.  
 DR InterPro; IPR001368; TNFR\_c6.  
 DR Pfam; PF00020; TNFR\_c6; 4.  
 DR PIRSF; PIRSF001968; TNFR\_2; 1.  
 DR SMART; SM00208; TNFR; 4.  
 DR PROSITE; PS00652; TNFR\_NGFR\_1; 2.  
 DR PROSITE; PS00650; TNFR\_NGFR\_2; 3.  
 KW Glycoprotein; Receptor; Repeat; Signal; Transmembrane.  
 FT SIGNAL 1 22  
 FT CHAIN 23 42 Tumor necrosis factor receptor superfamily member 1B.  
 FT DOMAIN 23 258 Extracellular (Potential).

FT TRANSMEM 259 288 Potential.  
 FT DOMAIN 289 474 Cytoplasmic (Potential).  
 FT REPEAT 39 77 TNFR-Cys 1.  
 FT REPEAT 78 119 TNFR-Cys 2.  
 FT REPEAT 120 164 TNFR-Cys 3.  
 FT REPEAT 165 203 TNFR-Cys 4.  
 FT DISULFID 40 54 By similarity.  
 FT DISULFID 55 68 By similarity.  
 FT DISULFID 58 76 By similarity.  
 FT DISULFID 79 94 By similarity.  
 FT DISULFID 97 111 By similarity.  
 FT DISULFID 101 119 By similarity.  
 FT DISULFID 121 127 By similarity.  
 FT DISULFID 136 145 By similarity.  
 FT DISULFID 139 163 By similarity.  
 FT DISULFID 166 181 By similarity.  
 FT CARBOHYD 69 69 N-linked (GlcNAc. .) (Potential).  
 FT CONFLICT 195 195 D -> DSDTVCAD (in Ref. 3).  
 FT CONFLICT 102 102 T -> S (in Ref. 3).  
 FT CONFLICT 108 108 I -> T (in Ref. 3).  
 FT CONFLICT 283 283 I -> F (in Ref. 3).  
 FT CONFLICT 331 331 S -> SS (in Ref. 3).  
 FT CONFLICT 360 360 F -> S (in Ref. 3).  
 FT CONFLICT 436 436 C -> Y (in Ref. 3).  
 SQ SEQUENCE 474 AA; 50319 MW; 462EAE398C4D6563 CRC64;  
 Query Match 26.0%; Score 295; DB 1; Length 474;  
 Best Local Similarity 34.0%; Pred. No. 7, 1e-17;  
 Matches 66; Conservative 24; Mismatches 84; Indels 20; Gaps 8;  
 QY 8 PYASE-NOTCRDQEKYEPQHRICCSPPGTYVSAKSRIDPTVCATCAENSNEHWN 66  
 DB 31 PKYPEPGYECQISQ-EYDRAQMCACRCPGQYVKHFCNKTSDTVCADCEASMTQVWN 89  
 QY 67 YLTICQLCR---PCDPVWGLSEIAPCTSKRKTQCRQCPQMCQA--AALECHTCELLSDC 121  
 DB 90 QFRTCLSCSSGCTTDQV----EIRACTQQRNVCAEAGRYCALKTHSGRCQCRLSKK 145  
 QY 122 PPGTEAEILKDEYGVKGNHCVCKAGHFQNTSSPSARCPQHTRCENQGLVEAAPGTQAQSDT 181  
 DB 146 GPGF-GVASSRAPNGVNLCKACAPTFSDTSSITDVCPRHICS-----ILAIPGNASTDA 200  
 QY 182 TCKNPLEPLPPEMS 195  
 DB 201 VC-----APESPTLS 210  
 RESULT 7  
 Q91ZM6  
 ID Q91ZM6 PRELIMINARY; PRT; 433 AA.  
 AC Q91ZM6;  
 DT 01-DEC-2001 (TRENBLrel. 19, Created)  
 DT 01-DEC-2001 (TRENBLrel. 19, Last sequence update)  
 DT 01-MAR-2004 (TRENBLrel. 26, Last annotation update)  
 DE Tumor necrosis factor receptor type II (fragment).  
 OS Rattus norvegicus (Rat).  
 OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;  
 OC Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Rattus.  
 OX NCBI\_TaxID=10116;  
 RN [1]  
 RP SEQUENCE FROM N.A.  
 RC STRAIN=Sprague-Dawley;  
 RX MEDLINE=22263089; PubMed=12376316;  
 RA Osburg B., Peiser C., Domling D., Schomburg L., Ko Y.T., Voigt K., Bickel U.;  
 RA "Effect of endotoxin on expression of TNF receptors and transport of TNF-alpha at the blood-brain barrier of the rat.";  
 RT Am. J. Physiol. Endocrinol. Metab. 283:E899-E908(2002).  
 RL EMBL; AF420214; AAL16021.1; -;  
 DR HSSP; P19438; INCF.  
 DR GO; GO:0004872; F:receptor activity; IEA.  
 DR Pfam; PF00020; TNFR\_c6; 2.

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DR SMART; SM00208; TNFR; 4.
DR PROSITE; PS00652; TNFR_NGFR_1; 2.
DR PROSITE; PS00505; TNFR_NGFR_2; 3.
KW Receptor.
FT NON_TER 1 433
FT NON_TER 433 433
SQ SEQUENCE 433 AA; 45723 MW; 75736DB35872C4A CRC64;

Query Match 25.7%; Score 291.5; DB 2; Length 433;
Best Local Similarity 33.3%; Pred. No. 1.3e-16;
Matches 65; Conservative 24; Mismatches 91; Indels 15; Gaps 7;

QY 8 PYASENQTCDQKEYYEYQHRCISRCPPGTYVSAKCSRIKDTVCATCAENSYNEHWY 67
DB 11 PYKPEPGNQCISQSEYDKKQMCCKACPPGGYAKHFCNKTSITVDCADCAAGMFTQVMNH 70
QY 68 LTICQLC-RPC--DPVWGLEETAPCTSKKTCRCQCPGMFCA--AWALECTHCELLSDCP 122
DB 71 LHTLSCSSSCSDQV----ETHNCTKQNRVCACNADSYCALKHLHSGNCRQCMKLSKCG 126
QY 123 PGTEAELKDEVGKNNHCVPCKAGHFQNTSSPSARCQPHTRCENQGLVEAAPGTAQSDTT 182
DB 127 PGF-GVARSRTSNGNVICSACAPGTFSDTTSSTDVCRPHRCS-----ILAIFGNASTDAV 181
QY 183 CKNPLEPLPPMSGT 197
DB 182 CASE-SPTPSAVPT 195

RESULT 8
Q6VAU8 PRELIMINARY; PRT; 461 AA.
AC Q6VAU8;
DT 05-JUL-2004 (TrEMBLrel. 27, Created)
DT 05-JUL-2004 (TrEMBLrel. 27, Last sequence update)
DT 05-JUL-2004 (TrEMBLrel. 27, Last annotation update)
DE Tumor necrosis factor receptor type 2 (Fragment).
OS Rattus norvegicus (Rat).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Rattus.
OX NCBI_TaxID=10116;
RN [1]
RP SEQUENCE FROM N.A.
RC STRAIN=Wistar; TISSUE=Spleen;
RA Inglis J.J., Chernajovsky Y., Kidd B.L.;
RL Submitted (JUL-2003) to the EMBL/GenBank/DBJ databases.
DR EMBL; AV344841; RAQ22350.1;
DR GO; GO:0016021; C:integral to membrane; IEA.
DR GO; GO:004872; F:receptor activity; IEA.
DR GO; GO:0005031; F:tumor necrosis factor receptor activity; IEA.
DR GO; GO:0019221; P:cytokine and chemokine mediated signaling p...; IEA.
DR InterPro; IPR001366; TNFR_c6.
DR Pfam; PF00020; TNFR_c6; 2.
DR SMART; SM00208; TNFR; 4.
DR PROSITE; PS00652; TNFR_NGFR_1; 2.
DR PROSITE; PS00505; TNFR_NGFR_2; 3.
KW Receptor.
FT NON_TER 1 461
FT NON_TER 461 461
SQ SEQUENCE 461 AA; 48857 MW; B36769C080B1308A CRC64;

Query Match 25.7%; Score 291.5; DB 2; Length 461;
Best Local Similarity 33.3%; Pred. No. 1.4e-16;
Matches 65; Conservative 24; Mismatches 91; Indels 15; Gaps 7;

QY 8 PYASENQTCDQKEYYEYQHRCISRCPPGTYVSAKCSRIKDTVCATCAENSYNEHWY 67
DB 25 PYKPEPGNQCISQSEYDKKQMCCKACPPGGYAKHFCNKTSITVDCADCAAGMFTQVMNH 84
QY 68 LTICQLC-RPC--DPVWGLEETAPCTSKKTCRCQCPGMFCA--AWALECTHCELLSDCP 122
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Db 95 LHTLSCSSSCSDQV----ETHNCTKQNRVCACNADSYCALKHLHSGNCRQCMKLSKCG 140
QY 123 PGTEAELKDEVGKNNHCVPCKAGHFQNTSSPSARCQPHTRCENQGLVEAAPGTAQSDTT 182
DB 141 PGF-GVARSRTSNGNVICSACAPGTFSDTTSSTDVCRPHRCS-----ILAIFGNASTDAV 195
QY 183 CKNPLEPLPPMSGT 197
DB 196 CASE-SPTPSAVPT 209

RESULT 9
TRIB_RAT
ID TRIB_RAT STANDARD; PRT; 474 AA.
AC Q80WY6;
DT 25-JAN-2005 (Rel. 46, Created)
DT 25-JAN-2005 (Rel. 46, Last sequence update)
DT 25-JAN-2005 (Rel. 46, Last annotation update)
DE Tumor necrosis factor receptor superfamily member 1B precursor (Tumor
DE necrosis factor receptor 2) (TNF-R2) (Tumor necrosis factor receptor
DE type II) (p75) (p80 TNF-alpha receptor).
GN Name=TNfrsf1b; Synonyms=TNfr2;
OS Rattus norvegicus (Rat).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Rattus.
OX NCBI_TaxID=10116;
RN [1]
RP SEQUENCE FROM N.A.
RC STRAIN=Wistar; TISSUE=Spleen;
RA Li Y., Ji A., Schafer M.K.;
RL Submitted (JUL-2003) to the EMBL/GenBank/DBJ databases.
CC -!- FUNCTION: Receptor with high affinity for TNFSP2/TNF-alpha and
CC approximately 5-fold lower affinity for homotrimeric
CC TNFSP1/lymphotoxin-alpha. The TRAF1/TRAF2 complex recruits the
CC apoptotic suppressors BIRC2 and BIRC3 to TNFRSF1B/TNFR2 (By
CC similarity).
CC -!- SUBUNIT: Binds to TRAF2 (By similarity).
CC -!- SUBCELLULAR LOCATION: Type I membrane protein (By similarity).
CC -!- SIMILARITY: Contains 4 TNFR-Cys repeats.
CC -----
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CC or send an email to license@sib-sib.ch).
CC -----
DR EMBL; AF498039; AAP33151.1; -.
DR HSP; P19438; INCF.
DR RGD; 621238; Tnfrsf1b.
DR InterPro; IPR001368; TNFR_c6.
DR InterPro; IPR011366; TNFR_c6; 2.
DR Pfam; PF00020; TNFR_c6; 2.
DR PIRSF; PIRSF001968; TNFR_2; 1.
DR SMART; SM00208; TNFR; 4.
DR PROSITE; PS00652; TNFR_NGFR_1; 2.
DR PROSITE; PS00505; TNFR_NGFR_2; 3.
KW Glycoprotein; Receptor; Repeat; Signal; Transmembrane.
FT SIGNAL 1 22
FT SIGNAL 22 22
FT CHAIN 23 474
FT CHAIN 23 474
FT DOMAIN 23 258
FT DOMAIN 258 288
FT TRANSMEM 289 474
FT DOMAIN 289 474
FT REPEAT 39 77
FT REPEAT 78 119
FT REPEAT 120 164
FT REPEAT 165 203
FT REPEAT 203 258
FT DISULFID 40 54
FT DISULFID 55 68
FT DISULFID 58 76
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FT	DISULFID	79	94	By similarity.	
FT	DISULFID	97	111	By similarity.	
FT	DISULFID	101	119	By similarity.	
FT	DISULFID	121	127	By similarity.	
FT	DISULFID	136	145	By similarity.	
FT	DISULFID	139	163	By similarity.	
FT	DISULFID	166	181	By similarity.	
FT	CARBOHYD	69	69	N-linked (GlcNAc. . .) (Potential).	
FT	CARBOHYD	110	110	N-linked (GlcNAc. . .) (Potential).	
FT	CARBOHYD	195	195	N-linked (GlcNAc. . .) (Potential).	
SQ	SEQUENCE	474 AA;	50148 MW;	239C6AB9B8C8D714 CRC64;	
	Query Match	25.7%;	Score 291.5;	DB 1;	Length 474;
	Best Local Similarity	33.3%;	Pred. No. 1.4e-16;		
	Matches	65;	Conservative	24;	Mismatches 91; Indels 15; Gaps 7;
Qy	8	PYASEN	TCRDQEXEYEPQHRICCSRCPPGYVS	AKSRIRDTVCATCAENS	YNEHWNY 67
Db	31	PYKPEPGNQCI	ISQYDYDKKAQMCCKCPGQYAKHFCN	KTSITVVCADCAAGMFTQVWNH 90	
Qy	68	LITCOLC-RPC	--DPVMGLBEBIACTSKRKTQCRQCPG	MFCF--AWALECTHCELLSDCP 122	
Db	91	LHTCLSCSSCSD	DDQV----ETHNCTKKQNRVCACNADYS	CALXKLHSGNCRCQMKLSKCG 146	
Qy	123	PGTEAEALKDEV	GKGNHNCVPCKAGCHFONTSPSARCOPH	TCECNOGLVEAAAPGTAQSDTT 182	
Db	147	PGF-GVARSRT	SGNVICSA	CAPTFSDTTSITDVC	PHRICS-----ILAI
Qy	183	CKNPLEPL	PEMSGT	197	
Db	202	CASE-SPTPS	AVPRT	215	

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RESULT 10
Q62327
ID ID Q62327 PRELIMINARY; PRT; 459 AA.
AC AC Q62327;
DT DT 01-NOV-1996 (TrEMBLrel. 01, Created)
DT DT 01-NOV-1996 (TrEMBLrel. 01, Last sequence update)
DT DT 01-OCT-2003 (TrEMBLrel. 25, Last annotation update)
DE DE Tumour necrosis factor receptor 2 protein (Fragment).
OS OS Name=Tnftrsf1b;
OS OS Mus musculus (Mouse).
OC OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC OC Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Mus.
NCBI_TaxID=10090;
[1]
RN RN SEQUENCE FROM N.A.
RC RC SEQUENCE=FROM N.A.
RC RC STRAIN=NOD;
RA RA Powell E.E., Wicker L.S., Peterson L.B., Todd J.A.;
RT RT "Amino acid variation in the tumor Necrosis factor receptor 2 is
RL RL linked to autoimmune diabetes in NOD mice.";
RN RN Genomics 0:0-0(0).
[2]
RN RN SEQUENCE FROM N.A.
RC RC SEQUENCE=FROM N.A.
RC RC STRAIN=NOD;
RX RX MEDLINE=95178848; PubMed=7873884;
RA RA Powell E.E., Wicker L.S., Peterson L.B., Todd J.A.;
RT RT "Allelic variation of the type 2 tumor necrosis factor receptor
RL RL gene.";
RL RL Mamm. Genome 5:726-727(1994).
DR DR EMBL; X76401; CAA53981.1; -.
DR DR PIR; I48854; I48854.
DR DR HSP; P19438; INCF.
DR DR MGD; MGII1314893; Tnftrsf1b.
DR DR CG; GO:0005615; C:extracellular space; TAS.
DR DR CG; GO:0016021; C:integral to membrane; TAS.
DR DR GO; GO:0008283; P:cell proliferation; TAS.
DR DR CG; GO:0007166; P:cell surface receptor linked signal transdu. .; IMP.
DR DR GO; GO:0006954; P:inflammatory response; IMP.
DR DR GO; GO:0008220; P:necrosis; IMP.
DR DR InterPro; IPR001368; TNFR c6.
DR DR Pfam; PF00020; TNFR c6; 2.

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DR	SMART; SMO0208; TNFR; 4.
DR	PROSITE; PS00652; TNFR_NGFR_1; 2.
DR	PROSITE; PS00050; TNFR_NGFR_2; 3.
KW	Receptor.
FT	NON TER.
FT	1
SQ	SEQUENCE 459 AA; 48686 MW; 6C51D2CF1C4626DF CRC64;
Query Match 25.6%; Score 290; DB 2; Length 459;	
Best Local Similarity 33.5%; Pred.No.1.8e-16;	
Matches 65; Conservative 24; Mismatches 85; Indels 20; Gaps 8;	
QY	8 PYASE-NQTCRDOEKEYEYPQHRIICSRCPPTGVVSAKSIRIDTVCATCAENSYNEHWN 66
DB	16 PYPEFGYEQIQSQ-EYYDRKAQCCKACPGQVYKHFCNKTSDTVCADCEASMYQTQWN 74
QY	67 YLTICQLCR---PCDPVMGLBEIAPTCTSKRTKTCRCOPGMFCA--AWALECTHCCELLSDC 121
DB	75 QFRTCLSCSSCSSTDQV-----ETRACTKQNVRVCACEAGRYCALKTHSGSRCQCMRLSKC 130
QY	122 PRGTAEALKEDEVGKNNHVCPVKAGHFQNTSSPSARCOPHTRCENQGLVEAPGTAQSDT 181
DB	131 GPGF-GVASSRAPNGNVLCACAPGTFSDTTSSTVDVCPHRICS----ILAIPGNASTDA 185
QY	182 TCKNPLEPLPPEMS 195
DB	186 VC----APESTPLS 195
RESULT 11	
TR6B HUMAN	
ID	TR6B_HUMAN STANDARD; PRT; 300 AA.
AC	O95407;
DT	28-FEB-2003 (Rel. 41, Created)
DT	28-FEB-2003 (Rel. 41, Last sequence update)
DT	05-JUL-2004 (Rel. 44, Last annotation update)
DE	Tumor necrosis factor receptor superfamily member 6B precursor (Decoy
DE	receptor for Fas ligand) (Decoy receptor 3) (DCR3) (M68)
DE	(UNQ186/PRO212).
OS	Name=TNFRSF6B; Synonyms=DCR3, TR6;
OS	Homo sapiens (Human)
OC	Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC	Mammalia; Eutheria; Primates; Catarrhini; Homnidae; Homo.
OX	NCBI_TaxID=9606;
RN	[1]
RN	SEQUENCE FROM N.A.
RP	TISSUE=Fetal lung;
RC	MEDLINE=9877321; PubMed=9877321; DOI=10.1038/25387;
RX	Pitti R.M., Marsters S.A., Lawrence D.A., Roy M., Kischkel P.C.,
RA	Dowd P., Huang A., Donahue C.J., Sherwood S.W., Baldwin D.T.,
RA	Godowski P.J., Wood W.I., Gurney A.B., Hillan K.J., Cohen R.L.,
RA	Goddard A.D., Botstein D., Ashkenazi A.;
RT	"Genomic amplification of a decoy receptor for Fas ligand in lung and
RT	colon cancer.";
RL	Nature 396:699-703(1998).
RN	[2]
RN	SEQUENCE FROM N.A., AND SEQUENCE OF 30-35.
RP	TISSUE=Prostate;
RC	MEDLINE=99253915; PubMed=99253915; DOI=10.1074/jbc.274.20.13733;
RX	Yu K.-Y., Kwon B., Ni J., Zhai Y., Ebner R., Kwon B.S.;
RA	"A newly identified member of tumor necrosis factor receptor
RT	superfamily (TR6) suppresses LIGHT-mediated apoptosis.";
RT	J. Biol. Chem. 274:13733-13736(1999).
RN	[3]
RN	SEQUENCE FROM N.A.
RP	TISSUE=Lung;
RC	MEDLINE=20122600; PubMed=10655513; DOI=10.1073/pnas.97.3.1230;
RX	Bai C., Connolly B., Metzger M.L., Hilliard C.A., Liu X., Sandig V.,
RA	Soderman A., Galloway S.M., Liu Q., Austin C.P., Caskey C.T.;
RA	"Overexpression of M68/Dcr3 in human gastrointestinal tract tumors
RT	independent of gene amplification and its location in a four-gene
RT	cluster.";
RL	Proc. Natl. Acad. Sci. U.S.A. 97:1230-1235(2000).
RN	[4]



RP SEQUENCE FROM N.A.  
 RX MEDLINE=22887296; PubMed=12975309; DOI=10.1101/gr.1293003;  
 RA Clark H.F., Gurney A.L., Abaya E., Baker K., Baldwin D., Brush J.,  
 RA Chen J., Chow B., Chui C., Crowley C., Currell B., Deuel B., Dowd P.,  
 RA Eaton D., Foster J., Grimaldi C., Gu Q., Hase P.E., Heldens S.,  
 RA Huang A., Kim H.S., Klimowski L., Jin Y., Johnson S., Lee J.,  
 RA Lewis L., Liao D., Mark M., Robbie E., Sanchez C., Schoenfeld J.,  
 RA Seshagiri S., Simmons L., Singh J., Smith V., Stinson J., Vagts A.,  
 RA Vandlen R., Watanabe C., Wiedand D., Woods K., Xie M.-H., Yansura D.,  
 RA Yi S., Yu G., Yuan J., Zhang M., Zhang Z., Goddard A., Wood W.I.,  
 RA Godowski P., Gray A.,  
 RT "The secreted protein discovery initiative (SPDI), a large-scale  
 RT effort to identify novel human secreted and transmembrane proteins: a  
 RT bioinformatics assessment.",  
 RL Genome Res. 13:2265-2270(2003).  
 [5]  
 RP SEQUENCE FROM N.A.  
 RX MEDLINE=21638749; PubMed=11780052; DOI=10.1038/414865a;  
 RA Deloukas P., Matthews L.H., Ashurst J.L., Burton J., Gilbert J.G.R.,  
 RA Jones M., Stavrides G., Almeida J.P., Babbage A.K., Bagguley C.L.,  
 RA Bailey J., Barlow K.F., Bates K.N., Beard L.M., Beare D.M.,  
 RA Beasley O.P., Bird C.P., Blakey S.E., Bridgeman A.M., Brown A.J.,  
 RA Buck D., Burrill W.D., Butler A.P., Carder C., Carter N.P.,  
 RA Chapman J.C., Clamp M., Clark G., Clark L.N., Clark S.Y., Clee C.M.,  
 RA Clegg S., Copley V.E., Collier R.E., Connor R.E., Corby N.R.,  
 RA Coulson A.G., Cowile G.J., Deadman R., Dhani P.D., Dunn M.,  
 RA Ellington A.G., Frankland J.A., Fraser A., French L., Garner P.,  
 RA Grafham D.V., Griffiths C., Griffiths M.N.D., Gwilliam R., Hall R.E.,  
 RA Hammond S., Harley J.B., Heath P.D., Ho S., Holden J.L., Howden P.J.,  
 RA Huckle E., Hunt A.R., Hunt S.E., Jekosch K., Johnson C.M., Johnson D.,  
 RA Kay M.P., Kimberley A.M., King A., Knights A., Laird G.K., Lawlor S.,  
 RA Leharvaish M.H., Leversha M.A., Lloyd C., Lloyd G.K., Lovell J.D.,  
 RA Marsh V.L., Martin S.L., McConachie L.J., McLay K., McMurray A.A.,  
 RA Milne S.A., Mistry D., Moore M.J.F., Mullikin J.C., Nickerson T.,  
 RA Oliver K., Parker A., Patel R., Pearce T.A.V., Peck A.I.,  
 RA Phillimore B.J.C.T., Prachalingam S.R., Plumb R.W., Ramsay H.,  
 RA Rice C.M., Ross M.T., Scott C.E., Sehra H.K., Showkneen R., Sims S.,  
 RA Skuce C.D., Smith M.L., Soderlund C., Steward C.A., Sulston J.E.,  
 RA Swann R.M., Sycamore N., Taylor R., Tee L., Thomas D.W., Thorpe A.,  
 RA Tracey A., Tromans A.C., Vaudin M., Wall M., Wallis J.M.,  
 RA Whitehead S.L., Whittaker P., Willey D.L., Williams L., Williams S.A.,  
 RA Wilming L., Wray P.W., Hubbard T., Durbin R.M., Bentley D.R., Beck S.,  
 RA Rogers J.;  
 RL "The DNA sequence and comparative analysis of human chromosome 20.";  
 RL Nature 414:865-871(2001).  
 [6]  
 RP SEQUENCE FROM N.A.  
 RC TISSUE=Lung, and Skin;  
 RX MEDLINE=22388257; PubMed=12477932; DOI=10.1073/pnas.242603899;  
 RA Strausberg R.L., Feingold E.A., Grouse L.H., Derge J.G.,  
 RA Klausner R.D., Collins F.S., Wagner F.S., Shenmen C.M., Schuler G.D.,  
 RA Altschul S.F., Zeeberg B., Buetow K.H., Schaefer C.F., Bhat N.K.,  
 RA Hopkins R.F., Jordan H., Moore T., Max S.I., Wang J., Hsieh F.,  
 RA Diatchenko L., Marusina K., Farmer A.A., Rubin G.M., Hong L.,  
 RA Stapleton M.J., Soares M.B., Bonaldi M.F., Casavant P., Prange C.,  
 RA Brownstein M.J., Ustin T.B., Toshiyuki S., Carninci P., Pange C.,  
 RA Raha S.S., Loquellano N.A., Peters G.J., Abramson R.D., Mullahy S.J.,  
 RA Bosak S.A., McSwan P.J., McKernan K.J., Malek J.A., Gunaratne P.H.,  
 RA Richards S., Worley K.C., Hale S., Garcia A.M., Gay L.J., Hulyk S.W.,  
 RA Vallalón D.K., Muny D.M., Sodergren E.J., Lu X., Gibbs R.A.,  
 RA Fahey J., Helton E., Kettelman M., Madan A., Rodrigues S., Sanchez A.,  
 RA Whiting M., Madan A., Young A.C., Shevchenko Y., Bouffard G.G.,  
 RA Blakesley R.W., Touchman J.W., Green E.D., Dickson M.C.,  
 RA Rodriguez A.C., Grimwood J., Schmutz J., Myers R.M.,  
 RA Butterfield Y.S.N., Krzywicki M.I., Skalska U., Smailus D.E.,  
 RA Schnerch A., Schein J.E., Jones S.J.M., Marra M.A.;  
 RT "Generation and initial analysis of more than 15,000 full-length human  
 RT and mouse cDNA sequences.";  
 RL Proc. Natl. Acad. Sci. U.S.A. 99:16899-16903(2002).  
 CC -!- FUNCTION: Decoy receptor for the cytotoxic ligands TNFSF14/LIGHT  
 CC and TNFSF6/FASL. Protects against apoptosis.  
 CC -!- SUBCELLULAR LOCATION: Secreted.  
 CC -!- TISSUE SPECIFICITY: Detected in fetal lung, brain and liver.

CC Detected in adult stomach, spinal cord, lymph node, trachea,  
 CC spleen, colon and lung. Highly expressed in several primary tumors  
 CC from colon, stomach, rectum, esophagus and in SW480 colon  
 CC carcinoma cells.  
 CC  
 CC -!- SIMILARITY: Contains 4 TNFR-Cys repeats.  
 CC  
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 CC or send an email to [license@isb-sib.ch](mailto:license@isb-sib.ch)).  
 CC  
 CC EMBL; AF104419; RAD03056.1; -  
 CC EMBL; AF134240; RAD29688.1; -  
 CC EMBL; AF217796; AAF35244.1; -  
 CC EMBL; AF217793; AAF33685.1; -  
 CC EMBL; AF217794; AAF33686.1; -  
 CC EMBL; AY358279; AAO88646.1; -  
 CC EMBL; AL121845; CAC03668.1; -  
 CC EMBL; BC017065; AAH17065.1; -  
 CC EMBL; BC034349; AAH34349.1; -  
 CC HSSP; O14763; 1DU3.  
 CC Genew; HGNC:11921; TNFRSF6B.  
 CC H-InvDB; HIX0016007; -  
 CC MIM; 603361; -  
 CC CO; GO:0005625; C:soluble fraction; TAS.  
 CC GO; GO:0004872; F:receptor activity; TAS.  
 CC GO; GO:0006916; P:anti-apoptosis; TAS.  
 CC InterPro; IPR009030; Grow\_fac\_recept.  
 CC InterPro; IPR001368; TNFR\_c6.  
 CC Pfam; PF00020; TNFR\_c6; 4.  
 CC SMART; SM00208; TNFR; 4.  
 CC PROSITE; PS00652; TNFR\_NGFR\_1; 1.  
 CC PROSITE; PS00500; TNFR\_NGFR\_2; 2.  
 KW Apoptosis; Direct protein sequencing; Glycoprotein; Receptor; Repeat;  
 FT SIGNAL.  
 FT CHAIN 1 29 Tumor necrosis factor receptor  
 FT REPEAT 30 300 superfamily member 6B.  
 FT REPEAT 31 70 TNFR-Cys 1.  
 FT REPEAT 72 113 TNFR-Cys 2.  
 FT REPEAT 115 150 TNFR-Cys 3.  
 FT REPEAT 152 193 TNFR-Cys 4.  
 FT DISULFID 49 62 By similarity.  
 FT DISULFID 52 70 By similarity.  
 FT DISULFID 73 88 By similarity.  
 FT DISULFID 91 105 By similarity.  
 FT DISULFID 95 113 By similarity.  
 FT DISULFID 115 126 By similarity.  
 FT DISULFID 132 150 By similarity.  
 FT DISULFID 153 168 By similarity.  
 FT DISULFID 174 193 By similarity.  
 FT CARBOHYD 173 173 N-linked (GlcNAc...) (Potential).  
 SQ SEQUENCE 300 AA; 32679 MW; F90AE33718449AF CRC64;  
 Query Match 25.2%; Score 285.5; DB 1; Length 300;  
 Best Local Similarity 36.0%; Pred. No. 2.9e-16;  
 Matches 63; Conservative 18; Mismatches 77; Indels 17; Gaps 7;  
 QY 25 BQHRICCSRCPPGTVVSAAKCSIRIDTVCATCAENSYNEHWNLYTICQLCRPCDPVWG-- 82  
 DB 42 ETGERLVCAQCPGGIFVORPCNRDSTTCGCPPPHYTQFMNLY---EKCRVCNVLGCR 98  
 QY 83 LEEIAPCTSKRTQCRCPGFMFC-AAWALECTHCELLSDCPGTEAEKLDKVGKGNHCV 141  
 DB 99 REEARACHATHNRACRCRTGFFAHAGFCL--H----ASCPEGA-GVIAPGTPSNTQCO 151  
 QY 142 PCKAGHFQNTSPSARCOPHTKCNQGLVEAAPGTAQSDTTCKN-----PLEPLPP 192  
 DB 152 PCPPGTTFSSSSSSSQCPHRCNCTALGLANALNPGSSSHDTLCTCTGTFPLTRVP 206

```

RESULT 12
Q7YRL5 QYRL5 PRELIMINARY; PRT; 274 AA.
AC QYRL5;
DT 01-OCT-2003 (TEMBLrel. 25, Created)
DT 01-OCT-2003 (TEMBLrel. 25, Last sequence update)
DT 01-MAR-2004 (TEMBLrel. 26, Last annotation update)
DE CD40.
GN Name=CD40;
OS Canis familiaris (Dog).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Carnivora; Fissipedia; Canidae; Canis.
OX NCBI_TaxID=9615;
RN [1]
SEQUENCE FROM N.A.
RA Yang S., SIm G.-K.;
RL Submitted (JUL-2003) to the EMBL/GenBank/DBJ databases.
DR EMBL; AY333789; AAP86653.1; -
DR HSP; P25942; 1FLI.
DR GO; GO:0004872; F:receptor activity; IEA.
DR InterPro; IPR001368; TNFR_C6.
DR Pfam; PF00020; TNFR_C6; 1.
DR SMART; SM00208; TNFR; 4.
DR PROSITE; PS00652; TNFR_NGFR_1; 1.
DR PROSITE; PS50050; TNFR_NGFR_2; 3.
SQ SEQUENCE 274 AA; 30284 MW; 9723789A07FAB6DB CRC64;

Query Match 25.1%; Score 284.5; DB 2; Length 274;
Best Local Similarity 34.9%; Pred. No. 3.2e-16;
Matches 61; Conservative 18; Mismatches 89; Indels 7; Gaps 4;

QY 9 YASENOTCDQEKYEPQHRICCSRCPPGTYSAKSIRDIVCAITCAENYHNVL 68
Db 19 YPEPTACR--EKQLVDSQ--CCNCPGEKLVNDCLHTIDTECTRCQTGFELDTWNAE 74
QY 69 TITQLCRCPDPVNGLEIEIAPCTSKRTQCRQCPGMFCAAWALECTHCELLSCPRTAE 128
Db 75 RHCHQHKYCDPLGLHVEKGTSETDTTCDEGLHCTWNA--CRSCTVHSLCPPLGVK 132
QY 129 LKDEVKGNHCVCPKAGHFONTSPSPACQPHTRCENQGLVEAAGFTAQSDTTC 183
Db 133 -QIATGISDTICDPCPGIFGFSNVSSALEKCHPWTSCETGLVKVQAGTKNTDVIC 186

RESULT 13
TR11_MOUSE
AC Q35305; Q8VCT7; STANDARD; PRT; 625 AA.
DT 16-OCT-2001 (Rel. 40, Created)
DT 16-OCT-2001 (Rel. 40, Last sequence update)
DT 05-JUL-2004 (Rel. 44, Last annotation update)
DE Tumor necrosis factor receptor superfamily member 11A precursor
DE (Receptor activator of NF-kB) (Osteoclast differentiation factor
DE receptor) (ODFR).
GN Name=Trnfrs11a; Synonyms=Rank;
OS Mus musculus (Mouse).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
OX NCBI_TaxID=10090;
RN [1]
SEQUENCE FROM N.A.
RP TISSUE=Fetal liver;
RC MEDLINE=98032977; PubMed=9367185; DOI=10.1038/36593;
RA Anderson D.M., Maraskovsky E., Billingsley W.L., Dougall W.C.,
RA Tometsko M.E., Roux E.R., Teepe M.C., DuBoise R.F., Cosman D.,
RA Galibert L.;
RT "A homologue of the TNF receptor and its ligand enhance T-cell growth
RT and dendritic-cell function."
RL Nature 390:175-179 (1997).
RN [2]
RP SEQUENCE FROM N.A.
RC TISSUE=Mammary gland;

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RX MEDLINE=22388257; PubMed=12477932; DOI=10.1073/pnas.242603899;
RA Strausberg R.L., Feingold E.A., Grouse L.H., Derge J.G.,
RA Klausner R.D., Collins F.S., Wagner L., Shenmen C.M., Schuler G.D.,
RA Altschul S.F., Zeeberg B., Buetow K.H., Schaefer C.F., Bhat N.K.,
RA Hopkins R.F., Jordan H., Moore T., Max S.I., Wang J., Hsieh P.,
RA Diatchenko L., Marusina K., Farmer A.A., Rubin G.M., Hong L.,
RA Stapleton M., Soares M.B., Bonaldo M.F., Caavaant T.L., Scheetz T.E.,
RA Brownstein M.J., Ussid T.B., Toshiyuki S., Carninci P., Prange C.,
RA Raha S.S., Loquellano N.A., Peters G.J., Abramson R.D., Mullahy S.J.,
RA Bosak S.A., McEwan P.J., McKernan K.J., Malek J.A., Gunaratne P.H.,
RA Richards S., Worley K.C., Hale S., Garcia A.M., Gay L.J., Hulyk S.W.,
RA Villalon D.K., Muzny D.M., Sodergren E.J., Lu X., Gibbs R.A.,
RA Fahy J., Helton E., Kettman M., Madan A.C., Rodriguez S., Sanchez A.,
RA Whiting M., Madan A., Young A.C., Shevchenko Y., Bouffard G.G.,
RA Blakesley R.W., Touchman J.W., Green E.D., Dickson M.C.,
RA Rodriguez A.C., Grimwood J., Schmutz J., Myers R.M.,
RA Butterfield Y.S.N., Krzywinski M.I., Skalska U., Smailus D.E.,
RA Schnerch A., Schein J.E., Jones S.J.M., Marra M.A.;
RT "Generation and initial analysis of more than 15,000 full-length human
RT and mouse cDNA sequences."
RL Proc. Natl. Acad. Sci. U.S.A. 99:16899-16903 (2002).
RN [3]
FUNCTION.
RP MEDLINE=99097247; PubMed=9878548; DOI=10.1006/bbrc.1998.9788;
RX Nakagawa N., Kinoshita M., Yamaguchi K., Shima N., Yasuda H., Yano K.,
RA Morinaga T., Higashio K.;
RT "RANK is the essential signaling receptor for osteoclast
RT differentiation factor in osteoclastogenesis."
RL Biochem. Biophys. Res. Commun. 253:395-400 (1998).
CC -!- FUNCTION: Receptor for TNFSF11/RANKL/TRANSC/OPGL; essential for
CC RANKL-mediated osteoclastogenesis. Involved in the regulation of
CC interactions between T-cells and dendritic cells.
CC -!- SUBUNIT: Interacts with TRAF1, TRAF2, TRAF3, TRAF5 and TRAF6 (By
CC similarity).
CC -!- SUBCELLULAR LOCATION: Type I membrane protein (Potential).
CC -!- TISSUE SPECIFICITY: Ubiquitous expression with high levels in
CC trabecular bone, thymus, small intestine, lung, brain and kidney.
CC Weakly expressed in spleen and bone marrow.
CC -!- SIMILARITY: Contains 4 TNFR-Cys repeats.
CC
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CC or send an email to license@isb-sib.ch).
CC
CC -----
CC EMBL; AF019046; AAB86810.1; -
CC EMBL; BC019185; AAH19185.1; -
CC HSP; O14763; IDU3.
CC MGD; MGI:1314891; Tnfrsf11a.
CC GO; GO:0007275; P:development; IMP.
CC GO; GO:0007515; P:lymph gland development; IMP.
CC GO; GO:0001503; P:ossification; IMP.
CC InterPro; IPR001368; TNFR_C6.
CC Pfam; PF00020; TNFR_C6; 3.
CC SMART; SM00208; TNFR; 4.
CC PROSITE; PS00652; TNFR_NGFR_1; 1.
CC PROSITE; PS50050; TNFR_NGFR_2; 1.
KW Glycoprotein; Receptor; Repeat; Signal; Transmembrane.
FT SIGNAL 1 30 Potential.
FT CHAIN 31 625 Tumor necrosis factor receptor
FT superfamily member 11A.
FT DOMAIN 31 214 Extracellular (Potential).
FT TRANSMEM 215 234 Potential.
FT DOMAIN 235 625 Cytoplasmic (Potential).
FT REPEAT 35 69 TNFR-Cys 1.
FT REPEAT 72 113 TNFR-Cys 2.
FT REPEAT 115 152 TNFR-Cys 3.
FT REPEAT 155 195 TNFR-Cys 4.
FT DISULFID 35 47 By similarity.
FT DISULFID 48 61 By similarity.

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FT DISULFID 51 69 By similarity.  
 FT DISULFID 72 87 By similarity.  
 FT DISULFID 93 113 By similarity.  
 FT DISULFID 115 128 By similarity.  
 FT DISULFID 134 152 By similarity.  
 FT CARBOHYD 106 106 N-linked (GlcNAc...) (Potential).  
 FT CARBOHYD 175 175 N-linked (GlcNAc...) (Potential).  
 FT CONFLICT 494 494 R -> K (in Ref. 2).  
 SQ SEQUENCE 625 AA; 66621 MW; F8C1872E99511D8E CRC64;

Query Match 25.0%; Score 283; DB 1; Length 625;  
 Best Local Similarity 32.6%; Pred. No. 9.6e-16;  
 Matches 60; Conservative 25; Mismatches 85; Indels 14; Gaps 4;

QY 4 QAVPPYASENQTCRQDEKEYEYFQHRICCSRCPPGTYVSAAKCSIRIDTVCATCAENSYNE 63  
 DB 30 QVTPPTQTE-----RHYEHLGR-CSCRCEPFGYLSKCTPTSDSVCLPCGPDPEYLD 79  
 QY 64 HNNYLTICQLCRPCDPVMGLEIEIAPCTSKRKTCQRCQPMFCMAALECTHCELLSDCPP 123  
 DB 80 TWNEEDKCLLHKVCDAGKALVADPGNHTAPRRCACCTAGYH---WNSDCCECCRRNTECAP 136  
 QY 124 GTEAEKLDKGVGNHNVCPCKAGHFQNTSSPSARCOPHTRCENQGLVEAAPGTAQSDTTC 183  
 DB 137 GFQAQHPQLNKL-DTVCCTPCLLGFSDVFSSTDKCPWTNCTLLGKLEAHQGTGTSDDVVC 195  
 QY 184 KNPL 187  
 DB 196 SSSN 199

RESULT 14  
 Q86YK5 PRELIMINARY; PRT; 223 AA.

ID Q86YK5  
 AC Q86YK5; 24, Created  
 DT 01-JUN-2003 (T-EMBLrel. 24, Last sequence update)  
 DT 01-JUN-2003 (T-EMBLrel. 24, Last sequence update)  
 DE 01-MAR-2004 (T-EMBLrel. 26, Last annotation update)  
 DE Tumor necrosis factor receptor superfamily member 5 (Fragment).  
 GN Name=TNFRSF5; Synonyms=CD40;  
 OS Homo sapiens (Human).  
 OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;  
 OC Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.  
 OC NCBI\_TaxID=9606;  
 RN [1]  
 RP SEQUENCE FROM N.A. (ISOFORM I).  
 RA He X., Xu L., Zeng Y.;  
 RA Submitted (JAN-2003) to the EMBL/GenBank/DBJ databases.  
 RL EMBL; AY225405; AAC43990.1; -;  
 DR HSSP; Q92956; IJMA.  
 DR GO; GO:0016020; C-membrane; IEA.  
 DR GO; GO:0004888; P:transmembrane receptor activity; IEA.  
 DR GO; GO:0006915; P:apoptosis; IEA.  
 DR GO; GO:0006955; P:immune response; IEA.  
 DR GO; GO:0007165; P:signal transduction; IEA.  
 DR InterPro; IPR006209; EGF like.  
 DR InterPro; IPR008063; Fas\_receptor.  
 DR InterPro; IPR001368; TNFR\_c6.  
 DR Pfam; PF000020; TNFR\_c6; 1.  
 DR PRINTS; PRO1680; FASRECEPTOR.  
 DR SMART; SM00208; TNFR; 4.  
 DR PROSITE; PS01186; EGF 2; UNKNOWN 1.  
 DR PROSITE; PS00652; TNFR\_NGFR\_1; 1.  
 DR PROSITE; PS50050; TNFR\_NGFR\_2; 4.  
 KW Receptor.  
 FT NON TER 223 223  
 SQ SEQUENCE 223 AA; 24659 MW; 85C63C20BC4E0B1C CRC64;

Query Match 24.5%; Score 278; DB 2; Length 223;  
 Best Local Similarity 35.0%; Pred. No. 9.3e-16;  
 Matches 62; Conservative 20; Mismatches 83; Indels 12; Gaps 5;

QY 7 PPVASENQTCRQDEKEYEYFQHRICCSRCPPGTYVSAAKCSIRIDTVCATCAENSYNEHW 66

Db 22 PPTA-----CR-EKYLINSQ--CCSLCQPKQKLVSDCTETFECLPCGESEFLDTWN 72  
 QY 67 YLTICQLCRPCDPVMGLEIEIAPCTSKRKTCQRCQPMFCMAALECTHCELLSDCPPGTE 126  
 Db 73 RETHCHQHKYCDPNLGLRVQOQGTSETDTICTCEGWHCTSEA--CESCVLHRS CSPGFG 130  
 QY 127 ASLKDEKGVGNHNVCPCKAGHFQNTSSPSARCOPHTRCENQGLVEAAPGTAQSDTTC 183  
 Db 131 VK-QIATGVSDTICEPCPGVGFPSNVSSAFKCHPWTSCETKDLVQOAGTKNTDVC 186

RESULT 15  
 TNRS HUMAN STANDARD; PRT; 277 AA.

ID TNRS HUMAN  
 AC P25942; O9BYU0;  
 DT 01-MAY-1992 (Rel. 22, Created)  
 DT 01-MAY-1992 (Rel. 22, Last sequence update)  
 DT 25-JAN-2005 (Rel. 46, Last annotation update)  
 DE Tumor necrosis factor receptor superfamily member 5 precursor (CD40L receptor) (B-cell surface antigen CD40) (CDw40) (Bp50).  
 GN Name=TNFRSF5; Synonyms=CD40;  
 OS Homo sapiens (Human).  
 OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;  
 OC Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.  
 OC NCBI\_TaxID=9606;  
 RN [1]  
 RP SEQUENCE FROM N.A. (ISOFORM I).  
 RA MEDLINE=89356608; PubMed=2475341;  
 RA Stamenkovic I., Clark E.A., Seed B.;  
 RA "A B-lymphocyte activation molecule related to the nerve growth factor receptor and induced by cytokines in carcinomas";  
 RL EMBO J. 8:1403-1410(1989).  
 RN [2]  
 RP SEQUENCE FROM N.A. (ISOFORM II).  
 RX MEDLINE=21117110; PubMed=11172023; DOI=10.1073/pnas.98.4.1751;  
 RA Tone M., Tone Y., Fairchild P.J., Wykes M., Waldmann H.;  
 RA "Regulation of CD40 function by its isoforms generated through alternative splicing";  
 RT Proc. Natl. Acad. Sci. U.S.A. 98:1751-1756(2001).  
 RN [3]  
 RP SEQUENCE FROM N.A. (ISOFORM I), AND VARIANTS LEU-124 AND ALA-227.  
 RA Livingston R.J., Rieder M.J., Chung M.-W., Ritchie T.K., Olson A.N.,  
 RA Nguyen C.P., Nguyen D.A., Poel C.L., Robertson P.D., Schackwitz W.S.,  
 RA Sherwood J.K., Sherwood A.M., Leithauer B.J., Nickerson D.A.;  
 RA "NIHES-SNPs, environmental genome project, NIHES ES15478, Department of Genome Sciences, Seattle, WA (URL: http://egp.gs.washington.edu).";  
 RL Submitted (DEC-2003) to the EMBL/GenBank/DBJ databases.  
 RN [4]  
 RP SEQUENCE FROM N.A.  
 RX MEDLINE=21638749; PubMed=11780052; DOI=10.1038/414865a;  
 RA Deloukas P., Matthews L.H., Ashurst J.L., Burton J., Gilbert J.G.R.,  
 RA Jones M., Stavrides G., Almeida J.P., Babbage A.K., Begguley C.L.,  
 RA Bailey J., Barlow K.F., Bates K.N., Beard L.M., Beare D.M.,  
 RA Beasley O.P., Bird C.P., Blakey S.E., Bridgeman A.M., Brown A.J.,  
 RA Buck D., Burrill W.D., Butler A.P., Carder C., Carter N.P.,  
 RA Chapman J.C., Clamp M., Clark G., Clark L.N., Clark S.V., Clee C.M.,  
 RA Clegg S., Cobley V.E., Collier R.E., Connor R.E., Corby N.R.,  
 RA Coulson A., Coville G.J., Deadman R., Dhani P.D., Dunn M.,  
 RA Ellington A.G., Frankland J.A., Fraser A., French L., Garner P.,  
 RA Grafham D.V., Griffiths C., Griffiths M.N.D., Gwilliam R., Hall R.E.,  
 RA Hammond S., Harley J.L., Heath P.D., Ho S., Holden J.L., Howden P.J.,  
 RA Huckle B., Hunt A.R., Hunt S.E., Jekosch K., Johnson C.M., Johnson D.,  
 RA Kay M.P., Kimberley A.M., King A., Knights A., Laird G.K., Lawlor S.,  
 RA Leharvalho M.H., Leversha M.A., Lloyd C., Lloyd D.M., Lovell J.D.,  
 RA Marsh V.L., Martin S.L., McConachie L.J., McClay K., McMurray A.A.,  
 RA Milne S.A., Mistry D., Moore M.J.F., Mullikin J.C., Nickerson T.,  
 RA Oliver K., Parker A., Patel R., Pearce T.A.V., Peck A.I.,  
 RA Phillimore B.J.C.T., Prathalingam S.R., Plumb R.W., Ramsay H.,  
 RA Rice C.M., Ross M.T., Scott C.E., Sehra H.K., Showkneen R., Sims S.,  
 RA Skuce C.D., Smith M.L., Soderlund C., Steward C.A., Sulston J.E.,  
 RA Swann R.M., Sycamore N., Taylor R., Tee L., Thomas D.W., Thorpe A.,  
 RA Tracey A., Tromans A.C., Vaudin M., Wall M., Wallis J.M.,

RA Whitehead S.L., Whittaker P., Willey D.L., Williams L., Williams S.A.,  
 RA Wilming L., Wray P.W., Hubbard T., Durbin R.M., Bentley D.R., Beck S.,  
 RA Rogers J.;  
 RT "The DNA sequence and comparative analysis of human chromosome 20.";  
 RA Nature 414:865-871(2001).  
 RN [5]  
 RN SEQUENCE FROM N.A. (ISOFORM I).  
 RC TISSUE=Ovary;  
 RX MEDLINE=22388257; PubMed=12477932; DOI=10.1073/pnas.242603899;  
 RA Klausberg R.L., Feingold E.A., Grouse L.H., Derge J.G.,  
 RA Krausner R.D., Collins F.S., Wagner L., Shermen C.M., Schuler G.D.,  
 RA Altschul S.F., Zeeberg B., Buetow K.H., Schaefer C.F., Bhat N.K.,  
 RA Hopkins R.F., Jordan H., Moore T., Max S.I., Wang J., Hsieh F.,  
 RA Diatchenko L., Marusina K., Farmer A.A., Rubin G.M., Hong L.,  
 RA Stapleton M., Soares M.B., Bonaldo M.F., Casavant T.L., Scheetz T.E.,  
 RA Brownstein M.J., Uedin T.B., Toshiyuki S., Carninci P., Prange C.,  
 RA Raha S.S., Loquellano N.J., Peters G.J., Abramson R.D., Mullahy S.J.,  
 RA Bosak S.A., McEwan P.J., McKernan K.J., Malek J.A., Gunaratne P.H.,  
 RA Richards S., Worley K.C., Hale S., Garcia A.M., Gay L.J., Hulyk S.W.,  
 RA Villalón D.K., Muzny D.M., Sodergren E.J., Lu X., Gibbs R.A.,  
 RA Fahey J., Helton E., Kettelman M., Madan A., Rodrigues S., Sanchez A.,  
 RA Whiting M., Madan A., Young A.C., Shevchenko Y., Bouffard G.G.,  
 RA Blakesley R.W., Touchman J.W., Green E.D., Dickson M.C.,  
 RA Rodriguez A.C., Grimwood J., Schmutz J., Myers R.M.,  
 RA Butterfield Y.S.N., Krzywinski M.I., Skalska U., Smallos D.E.,  
 RA Schnurch A., Schein J.E., Jones S.J.M., Warra M.A.;  
 RT "Generation and initial analysis of more than 15,000 full-length human  
 RT and mouse cDNA sequences.";  
 RL Proc. Natl. Acad. Sci. U.S.A. 99:16899-16903(2002).  
 RN [6]  
 RN SEQUENCE OF 21-30.  
 RP PubMed=11676606; DOI=10.1006/prep.2001.1501;  
 RX Khandekar S.S., Silverman C., Wells-Marani J., Bacon A.M., Birrell H.,  
 RA Brigham-Burke M., DeMarini D.J., Jonak Z.L., Camilleri P.,  
 RA Fishman-Loebell J.;  
 RT "Determination of carbohydrate structures N-linked to soluble CD154  
 RT and characterization of the interactions of CD40 with CD154 expressed  
 RT in Pichia pastoris and Chinese hamster ovary cells.";  
 RL Protein Expr. Purif. 23:301-310(2001).  
 RN [7]  
 RN SEQUENCE OF 21-35.  
 RP PubMed=15340161; DOI=10.1110/ps.04682504;  
 RX Zhang Z., Henzel W.J.;  
 RA "Signal peptide prediction based on analysis of experimentally  
 RT verified cleavage sites.";  
 RL Protein Sci. 13:2819-2824(2004).  
 RN [8]  
 RN INTERACTION WITH TRAF3.  
 RX MEDLINE=95184010; PubMed=7533327;  
 RA Cheng G., Cleary A.M., Ye Z.S., Hong D.I., Lederman S., Baltimore D.;  
 RT "Involvement of CRAF1, a relative of TRAF, in CD40 signaling.";  
 RL Science 267:1494-1498(1995).  
 RN [9]  
 RN INTERACTION WITH TRAF3.  
 RX MEDLINE=95129692; PubMed=7530216; DOI=10.1016/0014-5793(94)01406-Q;  
 RA Sato T., Irie S., Reed J.C.;  
 RT "A novel member of the TRAF family of putative signal transducing  
 RT proteins binds to the cytosolic domain of CD40.";  
 RL FEBS Lett. 358:113-118(1995).  
 RN [10]  
 RN INTERACTIONS WITH TRAF1, TRAF2, TRAF3 AND TRAF5.  
 RX MEDLINE=98384149; PubMed=9718306; DOI=10.1021/bi981067g;  
 RA Pullen S.S., Miller H.G., Everdeen D.S., Dang T.T., Crute J.J.,  
 RA Kehry M.R.;  
 RT "CD40-tumor necrosis factor receptor-associated factor (TRAF)  
 RT interactions: regulation of CD40 signaling through multiple TRAF  
 RT binding sites and TRAF hetero-oligomerization.";  
 RL Biochemistry 37:11836-11845(1998).  
 RN [11]  
 RN INTERACTION WITH TRAF5.  
 RX MEDLINE=98172745; PubMed=9511754; DOI=10.1016/S0378-1119(97)00616-1;  
 RA Mizushima S.-I., Fujita M., Ishida T., Azuma S., Kato K., Hirai M.,  
 RA Otsuka M., Yamamoto T., Inoue J.-I.;

RT "Cloning and characterization of a cDNA encoding the human homolog of  
 RT tumor necrosis factor receptor-associated factor 5 (TRAF5).";  
 RL Gene 207:135-140(1998).  
 RN [12]  
 RN INTERACTION WITH TRAF6.  
 RX MEDLINE=98095703; PubMed=9432981;  
 RA Kasbiwada M., Shirakata Y., Inoue J.-I., Nakano H., Okazaki K.,  
 RA Okumura K., Yamamoto T., Nagaoka H., Takemori T.;  
 RT "Tumor necrosis factor receptor-associated factor 6 (TRAF6) stimulates  
 RT extracellular signal-regulated kinase (ERK) activity in CD40 signaling  
 RT along a ras-independent pathway.";  
 RN J. Exp. Med. 187:237-244(1998).  
 RN [13]  
 RP 3D-STRUCTURE MODELING OF 24-144.  
 RX MEDLINE=97189482; PubMed=9037712;  
 RX DOI=10.1002/(SICI)1097-0134(199701)27:1<59::AID-PROT7>3.3.CO;2-Z;  
 RA Bajorath J., Aruffo A.;  
 RT "Construction and analysis of a detailed three-dimensional model of  
 RT the ligand binding domain of the human B cell receptor CD40.";  
 RL Proteins 27:59-70(1997).  
 RN [14]  
 RP 3D-STRUCTURE MODELING OF 26-186 IN COMPLEX WITH CD40L.  
 RX MEDLINE=98266353; PubMed=9605317;  
 RA Singh J., Garber E., van Vlijmen H., Karpusas M., Hsu Y.-M.,  
 RA Zheng Z., Naismith J.H., Thomas D.;  
 RT "The role of polar interactions in the molecular recognition of CD40L  
 RT with its receptor CD40.";  
 RL Protein Sci. 7:1124-1135(1998).  
 RN [15]  
 RP X-RAY CRYSTALLOGRAPHY (3.5 ANGSTROMS) OF 247-266 IN COMPLEX WITH  
 RP TRAF3.  
 RX MEDLINE=20442386; PubMed=10984535; DOI=10.1073/pnas.97.19.10395;  
 RA Ni C.Z., Welsh K., Leo E., Chlou C.K., Wu H., Reed J.C., Ely K.R.;  
 RT "Molecular basis for CD40 signaling mediated by TRAF3.";  
 RL Proc. Natl. Acad. Sci. U.S.A. 97:10395-10399(2000).  
 RN [16]  
 RP X-RAY CRYSTALLOGRAPHY (2.9 ANGSTROMS) OF 178-195 IN COMPLEX WITH  
 RP TRAF3.  
 RX MEDLINE=22000222; PubMed=12005438; DOI=10.1016/S0969-2126(02)00733-5;  
 RA Li C., Ni C.Z., Havert M.L., Cabezas E., He J., Kaiser D., Reed J.C.,  
 RA Satterthwait A.C., Cheng G., Ely K.R.;  
 RT "Downstream regulator TANK binds to the CD40 recognition site on  
 RT TRAF3.";  
 RL Structure 10:403-411(2002).  
 RN [17]  
 RP VARIANT HIGM3 ARG-83.  
 RX MEDLINE=21532985; PubMed=11675497; DOI=10.1073/pnas.221456898;  
 RA Ferrari S., Gilliani S., Insalaco A., Al-Ghonioum A., Sorsina A.R.,  
 RA Loubser M., Avanzini M.A., Marconi M., Badolato R., Ugazio A.G.,  
 RA Levy Y., Catalan N., Durandy A., Tbakhi A., Notarangelo L.D.,  
 RA Plebani A.;  
 RT "Mutations of CD40 gene cause an autosomal recessive form of  
 RT immunodeficiency with hyper IGM.";  
 RL Proc. Natl. Acad. Sci. U.S.A. 98:12614-12619(2001).  
 CC -!- FUNCTION: Receptor for TNFSF5/CD40L.  
 CC -!- SUBUNIT: Interacts with TRAF1, TRAF2, TRAF3, TRAF5 and TRAF6.  
 CC -!- SUBCELLULAR LOCATION: Type I membrane protein (isoform 1);  
 CC secreted (isoform II).  
 CC -!- ALTERNATIVE PRODUCTS:  
 CC Event=Alternative splicing; Named isoforms=2;  
 CC Comment=Additional isoforms seem to exist;  
 CC Name=I;  
 CC IsoId=P25942-1; Sequence=Displayed;  
 CC Name=II;  
 CC IsoId=P25942-2; Sequence=VSP\_006472, VSP\_006473;  
 CC -!- TISSUE SPECIFICITY: B-cells and in primary carcinomas.  
 CC -!- DISEASE: Defects in TNFSF5 are the cause of hyper-IGM  
 CC immunodeficiency type 3 (HIGM3) [MIM:606843]. HIGM3 is an

Query Match 24.5%; Score 278; DB 1; Length 277;  
 Best Local Similarity 35.0%; Pred. NO. 1.2e-15;  
 Matches 62; Conservative 20; Mismatches 83; Indels 12; Gaps 5;



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